

Sheppard, Paula

From: Portner, Ginny
Sent: Tuesday, December 10, 2002 4:05 PM
To: Sheppard, Paula
Subject: 09/369,992

Importance: High

Paula, I left a voice mail but am also sending an email. You completed a sequence search of nucleotides 1147-1740 of SEQ ID No 1, but I also need a oligomer search of this specific region as well. Do I need to resubmit an additional search request? G

Ginny Portner
CM1, Art Unit 1645
Room 7e13
Mail box 7e12
(703) 308-7543

*Interference
Search
done*

*OS
12/11/02*

Point of Contact
P. Sheppard
Telephone number: (703) 308-4496

12/13/02

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 20:27:43 ; Search time 2430 seconds
(without alignments)
3958.897 Million cell updates/sec

Title: US-09-369-992C-1_COPY_1147_1740
Perfect score: 594
Sequence: 1 gtagcgtttaatagcgaa.....ttacatctttcagcggtc 594

Scoring table: OLIGO_NUC
Gapop 60.0 , Capext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estnu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estcom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
 - 20: em_gss_pln:*
 - 21: em_gss_vrt:*
 - 22: em_gss_fun:*
 - 23: em_gss_mam:*
 - 24: em_gss_mus:*
 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	93	15.7	636	17	AZ525208
2	34	5.7	657	17	BH712144
3	34	5.7	706	17	BH515297
4	34	5.7	733	17	BH691669
5	34	5.7	739	17	BH461405
6	34	5.7	751	17	BH497288

7	34	5.7	797	17	BH420610
8	34	5.7	805	17	BH669801
c 9	33	5.6	121	17	BH593454
c 10	33	5.6	198	17	BH675598
c 11	33	5.6	210	17	BH735917
c 12	33	5.6	247	17	BH683107
c 13	33	5.6	263	17	BH492660
c 14	33	5.6	266	17	BH506879
c 15	33	5.6	269	17	BH728745
c 16	33	5.6	271	17	BH652699
c 17	33	5.6	275	17	BH603988
c 18	33	5.6	275	17	BH653527
c 19	33	5.6	284	17	BH739861
c 20	33	5.6	290	17	BH435779
c 21	33	5.6	290	17	BH697699
c 22	33	5.6	292	17	BH684204
c 23	33	5.6	309	17	BH015001
c 24	33	5.6	313	17	BH567920
c 25	33	5.6	319	17	BH599214
c 26	33	5.6	333	13	BJ235085
c 27	33	5.6	336	17	BH015002
c 28	33	5.6	336	17	BH655724
c 29	33	5.6	337	17	BH430665
c 30	33	5.6	342	9	AA948766
c 31	33	5.6	347	17	BH650187
c 32	33	5.6	351	17	BH463247
c 33	33	5.6	366	17	BH593989
c 34	33	5.6	370	17	BH720360
c 35	33	5.6	373	17	BH509392
c 36	33	5.6	377	13	BJ450787
c 37	33	5.6	381	10	AV556340
c 38	33	5.6	386	17	AQ843660
c 39	33	5.6	387	17	BH494088
c 40	33	5.6	388	17	BH694769
c 41	33	5.6	391	17	BH421905
c 42	33	5.6	399	17	BH662429
c 43	33	5.6	404	12	BF065393
c 44	33	5.6	404	17	BH142535
c 45	33	5.6	407	10	AV408731

ALIGNMENTS

RESULT 1
AZ525208/c
LOCUS 241PBD09 Pb MBN #21 Plasmodium berghei genomic 3', DNA sequence.
DEFINITION AZ525208
ACCESSION AZ525208
VERSION AZ525208.1 GI:13965828
KEYWORDS GSS.
SOURCE Plasmodium berghei.
ORGANISM Plasmodium berghei
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 636)
AUTHORS Carlton,J.M.-R. and Dame,J.B.
TITLE The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
COMMENT Contact: Dame JB
Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.vetmed.ufl.edu
Seq primer: M13(-20) forward
Class: shotgun.

FEATURES
source
Location/Qualifiers
1..636
/organism="Plasmodium berghei"
/strain="ANKA clone 15cyl (clone of the ANKA 8417 clone)"
/db_xref="taxon:5821"
/clone_lib="Pb MBN #21"

/dev_stages="asexual blood forms"
 /lab_host="Mus musculus"
 /note="Vector: pBluescript SK(+) vector DNA, phagemid
 excised from lambda ZAP; Site.1: EcoRV; Site.2: EcoRV;
 Genomic DNA was prepared from asynchronous blood stage
 forms of the cloned ANKA isolate of P. berghei grown in
 laboratory Swiss white mice. The DNA was purified from
 contaminating host DNA by Hoechst Dye 33258-CsCl
 ultracentrifugation and precipitated. Purified DNA was
 digested with mung bean nuclease in the presence of 36-38%
 formamide at 50 C, as described (Vernick, K.D., Imberski,
 R.B., and McCutchan, T.F. 1988. Nucleic Acids Research
 16:6883-6896). The ends of the digestion fragments were
 polished using T4 DNA polymerase, and the fragments size
 selected in the range 500-2000 bp. These were ligated into
 the EcoRV-cleaned and dephosphorylated pBluescript SK(+)
 vector. Recombinant plasmids were used to transform E.
 coli XL10-Gold host cells."

BASE COUNT 261 a 63 c 88 g 223 t 1 others
 ORIGIN

Query Match 15.7%; Score 93; DB 17; Length 636;
 Best Local Similarity 100.0%; Pred. No. 2.3e-30;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 502 TAATAAGAAATCTGCATCTTCACAGATAATTTTATTTCAATTAAGATTTTTTTTAAGAC 561
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 511 TAATAAGAAATCTGCATCTTCACAGATAATTTTATTTCAATTAAGATTTTTTTTAAGAC 452

QY 562 AGCAATTAAGTCGTACATCTTTCATGCAGGTC 594
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 451 AGCAATTAAGTCGTACATCTTTCATGCAGGTC 419

RESULT 2
 BH712144
 LOCUS BOMDQ17TR BO_2_3_KB Brassica oleracea genomic clone BOMDQ17, DNA
 DEFINITION
 ACCESSION BH712144
 VERSION BH712144.1 GI:18803004
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 657)
 Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished (2001)
 Other GSSs: BOMDQ17TF
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.

FEATURES
 source
 1..657
 /organism="Brassica oleracea"
 /strain="TC1000DH3"
 /db_xref="taxon:3712"
 /clone="BOMDQ17"

BASE COUNT 124 a 214 c 163 g 156 t

RESULT 4
 BH691669
 LOCUS BOMCZ07TF BO_2_3_KB Brassica oleracea genomic clone BOMCZ07, DNA
 DEFINITION
 ACCESSION BH691669.1 GI:18762106
 VERSION BH691669
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 733)
 Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea

Query Match 5.7%; Score 34; DB 17; Length 657;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 TAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 5 TAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 38

RESULT 3
 BH515297
 LOCUS BOHFD81TR BOHF Brassica oleracea genomic clone BOHFD81, DNA
 DEFINITION
 ACCESSION BH515297
 VERSION BH515297.1 GI:17723387
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 706)
 Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished (2001)
 Other GSSs: BOHFD81TF
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 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.

FEATURES
 source
 1..706
 /organism="Brassica oleracea"
 /strain="TC1000DH3"
 /db_xref="taxon:3712"
 /clone="BOHFD81"
 /note="vector: PHOS1; Site.1: BstXI; 2-3 kb sheared
 genomic DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 131 a 228 c 177 g 170 t

Query Match 5.7%; Score 34; DB 17; Length 706;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 TAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 29 TAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 62

RESULT 4
 BH691669
 LOCUS BOMCZ07TF BO_2_3_KB Brassica oleracea genomic clone BOMCZ07, DNA
 DEFINITION
 ACCESSION BH691669.1 GI:18762106
 VERSION BH691669
 KEYWORDS GSS.
 SOURCE Brassica oleracea.
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 733)
 Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea

JOURNAL
COMMENT

Unpublished (2001)
Other_GSSs: BOMC207TR
Contact: Chris Town
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Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES

source

Location/Qualifiers
1..733
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT 137 a 235 c 183 g 178 t

ORIGIN

Query Match 5.7%; Score 34; DB 17; Length 733;
Best Local Similarity 100.0%; Pred. NO. 0.00014;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 TAGCCCTGTTATCCCTAGAGTAAGTACTTTTATCCGTT 149

Db 32 TAGCCCTGTTATCCCTAGAGTAAGTACTTTTATCCGTT 65

RESULT 5

BH461405

LOCUS

DEFINITION BH461405 739 bp DNA linear GSS 13-DEC-2001
sequence.
BOGTM02TF BOGT Brassica oleracea genomic clone BOGTM02, DNA

ACCESSION

BH461405

VERSION

BH461405.1

GSS

KEYWORDS

SOURCE

ORGANISM

Brassica oleracea.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 739)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Other_GSSs: BOGTM02TR

Contact: Chris Town

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DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

FEATURES

source

Location/Qualifiers
1..739
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone_lib="BOGTM02"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT 138 a 234 c 188 g 179 t

ORIGIN

Query Match 5.7%; Score 34; DB 17; Length 739;
Best Local Similarity 100.0%; Pred. NO. 0.00014;

QY 116

TAGCCCTGTTATCCCTAGAGTAAGTACTTTTATCCGTT 149

Db 8

TAGCCCTGTTATCCCTAGAGTAAGTACTTTTATCCGTT 41

RESULT 6

BH497288

LOCUS

DEFINITION

BH497288

GSS

KEYWORDS

SOURCE

ORGANISM

Brassica oleracea.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 751)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Other_GSSs: BOHIU64TR

Contact: Chris Town

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DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

FEATURES

source

Location/Qualifiers
1..751
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone_lib="BOHIU64"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT 137 a 242 c 188 g 184 t

ORIGIN

Query Match 5.7%; Score 34; DB 17; Length 751;
Best Local Similarity 100.0%; Pred. NO. 0.00014;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 TAGCCCTGTTATCCCTAGAGTAAGTACTTTTATCCGTT 149

Db 32 TAGCCCTGTTATCCCTAGAGTAAGTACTTTTATCCGTT 65

RESULT 7

BH420610

LOCUS

DEFINITION

BH420610

GSS

KEYWORDS

SOURCE

ORGANISM

Brassica oleracea.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 797)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Contact: Chris Town

```

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Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
    source
        location/Qualifiers
            1..797
            /organism="Brassica oleracea"
            /strain="TO1000DH3"
            /db_xref="taxon:3712"
            /clone="BOHG03"
            /clone_lib="BOHG"
            /note="vector: pHOS1; site_1: BstXI; 2-3 kb sheared
            genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT    144 a   255 c   203 g   195 t
ORIGIN
Query Match          5.7%; Score 34; DB 17; Length 797;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 TAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
|||||
Db 29 TAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 62

RESULT 8
BH669801
LOCUS
DEFINITION
    BOMOU92TR BO_2_3_KB Brassica oleracea genomic clone BOMOU92, DNA
    sequence.
ACCESSION
    BH669801
VERSION
    BH669801.1 GI:18732275
KEYWORDS
    GSS.
SOURCE
    Brassica oleracea.
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
    1 (bases 1 to 805)
    Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
    Whole genome shotgun sequencing of Brassica oleracea
    Unpublished (2001)
    Contact: Chris Town
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
    source
        location/Qualifiers
            1..805
            /organism="Brassica oleracea"
            /strain="TO1000DH3"
            /db_xref="taxon:3712"
            /clone="BOMOU92"
            /clone_lib="BO_2_3_KB"
            /note="vector: pHOS1; site_1: BstXI; 2-3 kb sheared
            genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT    145 a   258 c   205 g   197 t
ORIGIN
Query Match          5.7%; Score 34; DB 17; Length 805;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 TAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
|||||

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Db 35 TAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 68

RESULT 9
BH593454/c
LOCUS
DEFINITION
    BH593454 BOHE Brassica oleracea genomic clone BOHE118, DNA
    sequence.
ACCESSION
    BH593454
VERSION
    BH593454.1 GI:17845906
KEYWORDS
    GSS.
SOURCE
    Brassica oleracea.
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
    1 (bases 1 to 121)
    Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
    Whole genome shotgun sequencing of Brassica oleracea
    Unpublished (2001)
    Other_GSSs: BOHE118TR
    Contact: Chris Town
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Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
    source
        location/Qualifiers
            1..121
            /organism="Brassica oleracea"
            /strain="TO1000DH3"
            /db_xref="taxon:3712"
            /clone="BOHE118"
            /clone_lib="BOHE"
            /note="vector: pHOS1; site_1: BstXI; 2-3 kb sheared
            genomic DNA inserted into pHOS1 using BstXI linkers"

BASE COUNT    28 a   32 c   35 g   26 t
ORIGIN
Query Match          5.6%; Score 33; DB 17; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
|||||
Db 53 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 21

RESULT 10
BH675598/c
LOCUS
DEFINITION
    BH675598 BOHf27TF BO_2_3_KB Brassica oleracea genomic clone BOHf27, DNA
    sequence.
ACCESSION
    BH675598
VERSION
    BH675598.1 GI:18745733
KEYWORDS
    GSS.
SOURCE
    Brassica oleracea.
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
    1 (bases 1 to 198)
    Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
    Whole genome shotgun sequencing of Brassica oleracea
    Unpublished (2001)
    Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208

```

Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES

source

Location/Qualifiers

1..198
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOHYF27"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

40 a 49 c 63 g 46 t

BASE COUNT

ORIGIN

Query Match 5.6%; Score 33; DB 17; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
|||||
Db 69 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 37

RESULT 11

BH735917

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 210)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOMBZ53TF
Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

Location/Qualifiers

1..210
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOMBZ53"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

48 a 68 c 50 g 44 t

BASE COUNT

ORIGIN

Query Match 5.6%; Score 33; DB 17; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
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Db 152 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 184

RESULT 12

BH683107/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 247)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOMLG07TF
Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

Location/Qualifiers

1..247
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOMLG07"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

61 a 64 c 80 g 42 t

BASE COUNT

ORIGIN

Query Match 5.6%; Score 33; DB 17; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
|||||
Db 197 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 165

RESULT 13

BH492660

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 263)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOHJC63TR
Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.

Location/Qualifiers

1..263
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOHJC63"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

263 bp DNA linear GSS 13-DEC-2001

BASE COUNT

ORIGIN

Query Match 5.6%; Score 33; DB 17; Length 263;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
|||||
Db 197 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 165

RESULT 14

BH683107

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 247)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOMLG07TF
Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

Location/Qualifiers

1..247
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOMLG07"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

61 a 64 c 80 g 42 t

BASE COUNT

ORIGIN

Query Match 5.6%; Score 33; DB 17; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
|||||
Db 197 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 165

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Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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  /organism="Brassica oleracea"
  /strain="TO1000DH3"
  /db_xref="taxon:3712"
  /clone="BOHJC63"
  /clone_lib="BOHJ"
  /note="vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"
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ORIGIN
Query Match      5.6%; Score 33; DB 17; Length 263;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
|||||
Db 177 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 209

RESULT 14
BH506879
LOCUS      BH506879 BOHKI70TR BOHK Brassica oleracea genomic clone BOHKI70, DNA
DEFINITION
sequence.
ACCESSION  BH506879
VERSION    BH506879.1 GI:17714976
KEYWORDS   GSS.
SOURCE     Brassica oleracea.
ORGANISM   Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 266)
AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE     Whole genome shotgun sequencing of Brassica oleracea
JOURNAL   Unpublished (2001)
COMMENT    Other_GSSs: BOHKI70TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
  1..266
  /organism="Brassica oleracea"
  /strain="TO1000DH3"
  /db_xref="taxon:3712"
  /clone="BOHKI70"
  /clone_lib="BOHK"
  /note="vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT      53 a   84 c   68 g   61 t
ORIGIN
Query Match      5.6%; Score 33; DB 17; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
|||||
Db 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149

RESULT 15
BH728745
LOCUS      BH728745 BO_2_3_KB Brassica oleracea genomic clone BOMMK86, DNA
DEFINITION
sequence.
ACCESSION  BH728745
VERSION    BH728745.1 GI:18834140
KEYWORDS   GSS.
SOURCE     Brassica oleracea.
ORGANISM   Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 269)
AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE     Whole genome shotgun sequencing of Brassica oleracea
JOURNAL   Unpublished (2001)
COMMENT    Other_GSSs: BOMMK86TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
  1..269
  /organism="Brassica oleracea"
  /strain="TO1000DH3"
  /db_xref="taxon:3712"
  /clone="BOMMK86"
  /clone_lib="BO_2_3_KB"
  /note="vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT      61 a   87 c   62 g   59 t
ORIGIN
Query Match      5.6%; Score 33; DB 17; Length 269;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
|||||
Db 218 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 250

Search completed: December 11, 2002, 22:11:03
Job time : 2437 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 20:30:23 ; Search time 69 Seconds
(without alignments)
2640.087 Million cell updates/sec

Title: US-09-369-992c-l_COPY_1147_1740

Perfect score: 594

Sequence: 1 gtagcgtttaatagcgaa.....ttacatcttctatgcaggtc 594

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
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5: /cgn2_6/ptodata/2/ina/PctUS_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27	4.5	2904	US-09-465-355-3	Sequence 3, Appli
C 2	25	4.2	1869	US-08-371-377-21	Sequence 21, Appl
C 3	24	4.0	294	US-09-134-001C-235	Sequence 235, App
C 4	24	4.0	294	US-09-134-001C-889	Sequence 889, App
C 5	24	4.0	294	US-09-134-001C-1038	Sequence 1038, Ap
C 6	24	4.0	294	US-09-134-001C-1355	Sequence 1355, Ap
C 7	24	4.0	294	US-09-134-001C-2007	Sequence 2007, Ap
C 8	24	4.0	321	US-09-134-001C-475	Sequence 475, App
C 9	24	4.0	8411	US-08-961-527-16	Sequence 16, Appl
C 10	23	3.9	3268	US-09-221-017B-981	Sequence 981, App
C 11	23	3.9	3901	US-09-221-017B-1043	Sequence 1043, Ap
C 12	23	3.9	4411529	US-09-103-840A-1	Sequence 1, Appli
C 13	22	3.7	2542	US-09-187-946-3	Sequence 3, Appli
C 14	20	3.4	1146	US-09-149-476-247	Sequence 247, App
C 15	20	3.4	1186	US-09-149-476-89	Sequence 89, Appl
C 16	20	3.4	1530	PCT-US96-05320A-899	Sequence 899, App
C 17	19	3.2	369	US-08-530-010-21	Sequence 21, Appl
C 18	19	3.2	369	US-08-484-101B-21	Sequence 21, Appl
C 19	19	3.2	369	US-08-714-524D-21	Sequence 21, Appl
C 20	19	3.2	740	US-08-998-416-771	Sequence 771, App
C 21	19	3.2	2787	US-08-530-010-2	Sequence 2, Appli
C 22	19	3.2	2787	US-08-530-010-4	Sequence 4, Appli
C 23	19	3.2	2787	US-08-530-010-6	Sequence 6, Appli
C 24	19	3.2	2787	US-08-530-010-8	Sequence 8, Appli
C 25	19	3.2	2787	US-08-530-010-10	Sequence 10, Appl
C 26	19	3.2	2787	US-08-484-101B-2	Sequence 2, Appli
C 27	19	3.2	2787	US-08-484-101B-4	Sequence 4, Appli

C 28	19	3.2	2787	1	US-08-484-101B-6	Sequence 6, Appli
C 29	19	3.2	2787	1	US-08-484-101B-8	Sequence 8, Appli
C 30	19	3.2	2787	1	US-08-484-101B-10	Sequence 10, Appl
C 31	19	3.2	2787	4	US-08-714-524D-2	Sequence 2, Appli
C 32	19	3.2	2787	4	US-08-714-524D-4	Sequence 4, Appli
C 33	19	3.2	2787	4	US-08-714-524D-6	Sequence 6, Appli
C 34	19	3.2	2787	4	US-08-714-524D-8	Sequence 8, Appli
C 35	19	3.2	2787	4	US-08-714-524D-10	Sequence 10, Appl
C 36	19	3.2	3552	4	US-09-157-210-3	Sequence 3, Appli
C 37	19	3.2	3567	2	US-09-166-203-1	Sequence 1, Appli
C 38	19	3.2	3567	4	US-09-377-309-1	Sequence 1, Appli
C 39	19	3.2	3879	1	US-08-530-010-1	Sequence 1, Appli
C 40	19	3.2	3879	1	US-08-484-101B-1	Sequence 1, Appli
C 41	19	3.2	3879	4	US-08-714-524D-1	Sequence 1, Appli
C 42	18	3.0	207	4	US-09-134-001C-239	Sequence 239, App
C 43	18	3.0	207	4	US-09-134-001C-498	Sequence 498, App
C 44	18	3.0	207	4	US-09-134-001C-893	Sequence 893, App
C 45	18	3.0	207	4	US-09-134-001C-1061	Sequence 1061, Ap

ALIGNMENTS

RESULT 1

US-09-465-355-3/C
; Sequence 3, Application US/09465355
; Patent No. 6316194

; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan

; APPLICANT: Knowles, David

; APPLICANT: Murchie, Alastair

; APPLICANT: Lentzen, Georg

; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Antimicrobials

; FILE REFERENCE: 22620/1150 (Formerly 3950/85276)

; CURRENT APPLICATION NUMBER: US/09/465,355

; CURRENT FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: US 09/325,601

; PRIOR FILING DATE: 1999-06-03

; PRIOR APPLICATION NUMBER: GB 9812196.5

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: GB 9904790.4

; PRIOR FILING DATE: 1999-03-02

; PRIOR APPLICATION NUMBER: US 60/122,439

; PRIOR FILING DATE: 1999-03-02

; PRIOR APPLICATION NUMBER: US 60/088,241

; PRIOR FILING DATE: 1998-06-05

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 2904

; TYPE: RNA

; ORGANISM: Escherichia coli

US-09-465-355-3

Query Match 4.5%; Score 27; DB 4; Length 2904;

Best Local Similarity 100.0%; Pred. No. 0.0027;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 TAGGAGGAGACGCCCGCAGTCAAACTA 313

|||||

Db 2267 TAGGAGGAGACGCCCGCAGTCAAACTA 2241

RESULT 2

US-08-371-377-21/c

; Sequence 21, Application US/08371377

; Patent No. 5851764

; GENERAL INFORMATION:

; APPLICANT: Fisher, Paul B.

; APPLICANT: Shen, Ruqian

; TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND

; TITLE OF INVENTION: IMMUNOLOGICAL REAGENTS SPECIFIC FOR CELL SURFACE-EXPRESSED

; TITLE OF INVENTION: MOLECULES AND TRANSFORMATION-ASSOCIATED GENES

NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,377
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/37590-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1869 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-371-377-21

Query Match 4.0%; Score 25; DB 2; Length 1869;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGTGCCAAACCTT 87
|||||
DB 1759 AGCCGACATCGAGTGCCAAACCTT 1735

RESULT 3

US-09-134-001C-235/c
Sequence 235, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134, 001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 235
LENGTH: 294
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-235

Query Match 4.0%; Score 24; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGTGCCAAACCTT 86
|||||
DB 175 AGCCGACATCGAGTGCCAAACCTT 152

RESULT 4

US-09-134-001C-889/c
Sequence 889, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134, 001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 889
LENGTH: 294
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-889

Query Match 4.0%; Score 24; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGTGCCAAACCTT 86
|||||
DB 175 AGCCGACATCGAGTGCCAAACCTT 152

RESULT 5

US-09-134-001C-1038/c
Sequence 1038, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134, 001C
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1038
LENGTH: 294
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1038

Query Match 4.0%; Score 24; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGTGCCAAACCTT 86
|||||
DB 175 AGCCGACATCGAGTGCCAAACCTT 152

RESULT 6

US-09-134-001C-1355/c
Sequence 1355, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1355
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1355

Query Match 4.0%; Score 24; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGGTGCCAAACCT 86
|||||
Db 175 AGCCGACATCGAGGTGCCAAACCT 152

RESULT 7

US-09-134-001C-2007/c
; Sequence 2007, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2007
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2007

Query Match 4.0%; Score 24; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGGTGCCAAACCT 86
|||||
Db 175 AGCCGACATCGAGGTGCCAAACCT 152

RESULT 8

US-09-134-001C-475/c
; Sequence 475, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 475
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-475

Query Match 4.0%; Score 24; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGGTGCCAAACCT 86
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Db 175 AGCCGACATCGAGGTGCCAAACCT 152

RESULT 9

US-08-961-527-16/c
; Sequence 16, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: P8340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-16

Query Match 4.0%; Score 24; DB 4; Length 8411;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGGTGCCAAACCT 86
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Db 32 AGCCGACATCGAGGTGCCAAACCT 9

RESULT 10

US-09-221-017B-981
; Sequence 981, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD

CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 981:
SEQUENCE CHARACTERISTICS:
LENGTH: 3268 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...3268
US-09-221-017B-981

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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGTGCCAAACC 85
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DB 2896 AGCCGACATCGAGTGCCAAACC 2918

RESULT 11

US-09-221-017B-1043/c
Sequence 1043, Application US/09221017B
Patent No. 644799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1043:
SEQUENCE CHARACTERISTICS:
LENGTH: 3901 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...3901
US-09-221-017B-1043

Query Match 3.9%; Score 23; DB 4; Length 3901;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGTGCCAAACC 85
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DB 1902 AGCCGACATCGAGTGCCAAACC 1880

RESULT 12

US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA

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; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

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Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGGTGCCAAACC 85
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Db 1476404 AGCCGACATCGAGGTGCCAAACC 1476382

RESULT 13
US-09-187-946-3/C
; Sequence 3, Application US/09187946
; Patent No. 6255467
; GENERAL INFORMATION:
; APPLICANT: Lindner, Luther E.
; APPLICANT: Macphree, Kathleen
; TITLE OF INVENTION: Human Blood Bacterium
; FILE REFERENCE: D6026
; CURRENT APPLICATION NUMBER: US/09/187,946
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: US 60/064,472
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 3
; LENGTH: 2542
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: Rb 23S rRNA sequence of a new human blood bacterium
US-09-187-946-3

; Query Match          3.7%; Score 22; DB 4; Length 2542;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCCGACATCGAGGTGCCAAAC 84
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Db 2311 AGCCGACATCGAGGTGCCAAAC 2290

RESULT 14
US-09-149-476-247/C
; Sequence 247, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
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; EARLIER APPLICATION NUMBER: 60/056,893
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,630
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,878
 ; EARLIER FILING DATE: 1997-08-22
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 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,872
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 ; EARLIER FILING DATE: 1997-08-22
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 ; EARLIER APPLICATION NUMBER: 60/056,911
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,636
 ; EARLIER FILING DATE: 1997-08-22
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 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,910
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,864
 ; EARLIER FILING DATE: 1997-08-22
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 ; EARLIER FILING DATE: 1997-08-22
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 ; EARLIER FILING DATE: 1997-08-22
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 ; EARLIER APPLICATION NUMBER: 60/057,761
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/047,595
 ; EARLIER FILING DATE: 1997-05-23
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 ; EARLIER FILING DATE: 1997-05-23
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 ; EARLIER APPLICATION NUMBER: 60/047,594
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,589
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,593
 ; EARLIER FILING DATE: 1997-05-23
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 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/043,578
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/043,576
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/047,501
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/043,670
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/056,632
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,664

; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,876
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,881
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,909
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,875
 ; EARLIER FILING DATE: 1997-08-22
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 ; EARLIER APPLICATION NUMBER: 60/056,908
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/048,964
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/057,650
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER APPLICATION NUMBER: 60/056,884
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/057,669
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER APPLICATION NUMBER: 60/049,610
 ; EARLIER FILING DATE: 1997-06-13
 ; EARLIER APPLICATION NUMBER: 60/061,060
 ; EARLIER FILING DATE: 1997-10-02

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 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 234 TATATATTTTATCTTTATATA 253
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 Db 481 TATATATTTTATCTTTATATA 462

 RESULT 15
 US-09-149-476-89/c
 ; Sequence 89, Application US/09149476
 ; Patent No. 6420526
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: P2002P1
 ; CURRENT APPLICATION NUMBER: US/09/149,476
 ; CURRENT FILING DATE: 1998-09-08
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493
 ; EARLIER FILING DATE: 1998-03-06
 ; EARLIER APPLICATION NUMBER: 60/040,162
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,333
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/038,621
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,626
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 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,615
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 ; EARLIER APPLICATION NUMBER: 60/047,502
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/	EARLIER APPLICATION NUMBER:	60/056,864
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/057,650
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; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          3.48; Score 20; DB 4; Length 1186;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 534 TATATATTTATCTTTATATA 515
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Job time : 2898 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 19:01:38 ; Search time 304 Seconds
(without alignments)
4400.286 Million cell updates/sec

Title: US-09-369-992C-l_COPY_1147_1740

Perfect score: 594

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Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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3	33	5.6	134525	11	AAQ04525		Total base sequenc
c	4	27	4.5	638	22	AAC89401	E.coli 23S rRNA DN
c	5	27	4.5	813	23	AAS82419	DNA encoding novel
c	6	27	4.5	1258	24	AAK99200	1258nt of E-site R
c	7	27	4.5	1446	23	AAS87232	DNA encoding novel
c	8	27	4.5	2115	23	AAS77887	DNA encoding novel
9	27	4.5	2904	21	AAA66047		E. coli proliferat

10	27	4.5	2904	21	AAAG6052	E. coli proliferat	
c	11	27	4.5	2904	22	AAH75411	E. coli 23S rRNA.
c	12	27	4.5	2904	22	AAE23016	E. coli 23S rRNA.
c	13	27	4.5	2904	22	AAC89403	Sequences from 23S
c	14	27	4.5	2907	19	AAV38096	Enterohaemorrhagic
c	15	27	4.5	2907	19	AAV38107	Enterohaemorrhagic
16	27	4.5	2910	23	AA82418	DNA encoding novel	
17	27	4.5	2910	23	AA82418	DNA encoding novel	
c	18	27	4.5	2958	23	AA86736	DNA encoding novel
c	19	27	4.5	3067	23	AA89786	DNA encoding novel
c	20	27	4.5	3118	22	AAH49806	Escherichia coli t
c	21	27	4.5	3687	23	AA890090	DNA encoding novel
22	27	4.5	3756	23	AA893772	DNA encoding novel	
c	23	27	4.5	5013	20	AA824985	E. coli MG1655 rrr
c	24	27	4.5	5014	20	AA824987	E. coli MG1655 rrr
c	25	27	4.5	5090	20	AA824988	E. coli MG1655 rrr
c	26	27	4.5	5097	20	AA824983	E. coli MG1655 rrr
c	27	4.5	5098	20	AA824984	E. coli MG1655 rrr	
c	28	27	4.5	5105	20	AA824989	E. coli MG1655 rrr
c	29	27	4.5	5162	23	AA888865	E. coli MG1655 rrr
30	27	4.5	5341	20	AA824986	DNA encoding novel	
c	31	27	4.5	105184	24	ABK24122	E. coli MG1655 rrr
32	27	4.5	269223	22	AAE28554	Bacterial artifi	
33	25	4.2	444	13	AAQ31812	Genomic fragmen	
c	34	25	4.2	1869	17	AAT37413	Astrovirus serotyp
c	35	25	4.2	2940	24	ABL54765	Prostate tumour in
c	36	25	4.2	5273	20	AA824982	Lactobacillus plan
c	37	25	4.2	5519	20	AA824981	Haemophilus influe
38	25	4.2	640681	24	ABA92787	Haemophilus influe	
39	25	4.2	1830121	17	AA824063	Buchnera sp. genom	
40	24	4.0	24	19	AAV33153	Haemophilus influe	
c	41	24	4.0	55	18	AAV79333	Plasmodium berghei
42	24	4.0	97	23	AA50394	Staphylococcus aur	
43	24	4.0	120	18	AAV79107	Staphylococcus aur	
44	24	4.0	135	18	AAV79076	Staphylococcus aur	
45	24	4.0	136	18	AAV79080	Staphylococcus aur	

ALIGNMENTS

RESULT 1
AAV33135
ID AAV33135 standard; DNA; 5849 BP.
XX AAV33135;
AC AAV33135;
XX
DT 07-DEC-1998 (first entry)
XX Plasmodium berghei plasmid PSL-PLA70 gene.
DE Malaria; infection; therapy; diagnosis; vaccine; plasmid;
KW PSL-PLA70 gene; ds.
XX Plasmodium berghei ANKA strain.
OS
XX WO9835057-A1.
PN
XX 13-AUG-1998.
PD
XX 05-FEB-1998; 98WO-IB00212.
PF
XX 26-SEP-1997; 97AU-0009481.
PR
XX 06-FEB-1997; 97AU-0004953.
PR
XX 21-APR-1997; 97AU-0006329.
XX (MOLE-) INST MOLECULAR & CELL BIOLOGY.
XX (UYSI-) UNIV SINGAPORE NAT.
PI Kara AKU, Nelson JS, Tan TMC, Tham JM, Ting RCY;
XX WPI; 1998-447251/38.
XX

PT Detecting Plasmodium infection from hybridisation with
 PT extrachromosomal element - providing humans or species specific
 PT diagnosis with few false negatives, in humans or animals
 XX
 PS Claim 15; Page 54-59; 120pp; English.

XX This is the nucleotide sequence of one strand of the PSL-PL470
 CC gene of the 30.7 kb extrachromosomal plasmid of Plasmodium berghei.
 CC This plasmid encodes organelle-like rRNAs, tRNAs, ribosomal
 CC proteins and RNA polymerase subunits, amongst others. Plasmodium is
 CC detected in a human or animal sample by treating it, or derived
 CC nucleic acid, with a Plasmodium extrachromosomal genetic element or
 CC derived nucleic acid (A) and detecting any hybridisation. (A) can
 CC include the PSL-PL470, PLH-PPH, PRB or PMQ gene, the mitochondrial
 CC coxI gene, and nucleic acids derived from them. Also new are
 CC (A)-specific probes and primers (see AAV3139-56). The method is
 CC used to diagnose Plasmodium infection. Also (not claimed) the
 CC polypeptides encoded by (A) are useful as targets for drug
 CC development and for development of anti-malaria vaccines. The high
 CC degree of similarity between (A) from different species allows
 CC development of genus- or species-specific assays that result in
 CC fewer false negatives than known methods (typically 1% against 3%).
 XX

XX Sequence 5849 BP; 2296 A; 673 C; 557 G; 2323 T; 0 other;

Query Match 100.0%; Score 594; DB 19; Length 5849;
 Best Local Similarity 100.0%; Pred. No. 3.6e-261;
 Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTATCGCTTTAATAGGCGACAGACTTACCTTAAACATACACTACTGCTTAGGATCGGA 60
 Db 1147 GTATCGCTTTAATAGGCGACAGACTTACCTTAAACATACACTACTGCTTAGGATCGGA 1206

Qy 61 TAAGCGACATCGAGGTCGCAACCTTTTCGTCATATGACCTCGGAAAGATAGCC 120
 Db 1207 TAAGCGACATCGAGGTCGCAACCTTTTCGTCATATGACCTCGGAAAGATAGCC 1266

Qy 121 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTAATAAATATATCG 180
 Db 1267 TGTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTAATAAATATATCG 1326

Qy 181 GATCATTAAGACCGACATTAATCTCTGTTAAATTTTACAGTTAAATATATAT 240
 Db 1327 GATCATTAAGACCGACATTAATCTCTGTTAAATTTTACAGTTAAATATATAT 1386

Qy 241 TTATCTTTATATAATAATAATTAACATTTGACCTCGTTTTTATATAGGAGGAGACCGC 300
 Db 1387 TTATCTTTATATAATAATAATTAACATTTGACCTCGTTTTTATATAGGAGGAGACCGC 1446

Qy 301 CCCAGTCAAACTATCTTATAAATATTTGTTATAAATAATTTTATAAGAAT 360
 Db 1447 CCCAGTCAAACTATCTTATAAATATTTGTTATAAATAATTTTATAAGAAT 1506

Qy 361 TTATATATATAAATAAGGTTATTCATTAACAATACATTTATCCAAAAATAATATT 420
 Db 1507 TTATATATATAAATAAGGTTATTCATTAACAATACATTTATCCAAAAATAATATT 1566

Qy 421 ACTACTCCCATTTTATCTGTATATATATATATTTTCAATATCTATTAATAGTAAG 480
 Db 1567 ACTACTCCCATTTTATCTGTATATATATATATTTTCAATATCTATTAATAGTAAG 1626

Qy 481 CTTCATAGGGTCTTCTGTCTATATAAAGAAATTCGATCTTCACAGATAATTTTATTT 540
 Db 1627 CTTCATAGGGTCTTCTGTCTATATAAAGAAATTCGATCTTCACAGATAATTTTATTT 1686

Qy 541 CATTAAGATTTTTTTTAAAGACAGATTTAAGTCGTTACATCTTTCATGCAGGTC 594
 Db 1687 CATTAAGATTTTTTTTAAAGACAGATTTAAGTCGTTACATCTTTCATGCAGGTC 1740

RESULT 2
 AAQ04525
 ID AAQ04525 standard; DNA; 134525 BP.

XX AAQ04525;
 AC 01-OCT-1990 (first entry)
 DT
 XX Total base sequence of rice plant chloroplast DNA.
 DE
 XX Chloroplast; true grass; rice plant; ss.
 KW
 XX Oryza sativa.
 OS
 XX JP02100682-A.
 PN
 XX 12-APR-1990.
 PD
 XX 07-OCT-1988; 88JP-0251967.
 PF
 XX 07-OCT-1988; 88JP-0251967.
 PR
 XX (MITK) MITSUI TOATSU CHEM INC.
 PA
 XX WPI; 1990-159709/21.
 DR
 XX

PT Chloroplast DNA of true grasses - used to produce various
 PT DNA base sequences by decomposition of rice plant DNA.

PS Claim 1; Fig 1; 20pp; Japanese.

CC The sequence is that of the whole of rice chloroplast DNA.

XX Sequence 134525 BP; 41249 A; 26129 C; 26331 G; 40816 T; 0 other;

Query Match 5.6%; Score 33; DB 11; Length 134525;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
 Db 117355 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 117387

RESULT 3
 AAQ04525/c
 ID AAQ04525 standard; DNA; 134525 BP.

XX AAQ04525;
 AC 01-OCT-1990 (first entry)
 DT
 XX Total base sequence of rice plant chloroplast DNA.
 DE
 XX Chloroplast; true grass; rice plant; ss.
 KW
 XX Oryza sativa.
 OS
 XX JP02100682-A.
 PN
 XX 12-APR-1990.
 PD
 XX 07-OCT-1988; 88JP-0251967.
 PF
 XX 07-OCT-1988; 88JP-0251967.
 PR
 XX (MITK) MITSUI TOATSU CHEM INC.
 PA
 XX WPI; 1990-159709/21.
 DR
 XX

PT Chloroplast DNA of true grasses - used to produce various
 PT DNA base sequences by decomposition of rice plant DNA.

PS Claim 1; Fig 1; 20pp; Japanese.

CC The sequence is that of the whole of rice chloroplast DNA.

XX Sequence 134525 BP; 41249 A; 26129 C; 26331 G; 40816 T; 0 other;

Query Match 5.6%; Score 33; DB 11; Length 134525;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
 Db 117355 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 117387

RESULT 3
 AAQ04525/c
 ID AAQ04525 standard; DNA; 134525 BP.

XX AAQ04525;
 AC 01-OCT-1990 (first entry)
 DT
 XX Total base sequence of rice plant chloroplast DNA.
 DE
 XX Chloroplast; true grass; rice plant; ss.
 KW
 XX Oryza sativa.
 OS
 XX JP02100682-A.
 PN
 XX 12-APR-1990.
 PD
 XX 07-OCT-1988; 88JP-0251967.
 PF
 XX 07-OCT-1988; 88JP-0251967.
 PR
 XX (MITK) MITSUI TOATSU CHEM INC.
 PA
 XX WPI; 1990-159709/21.
 DR
 XX

PT Chloroplast DNA of true grasses - used to produce various
 PT DNA base sequences by decomposition of rice plant DNA.

PS Claim 1; Fig 1; 20pp; Japanese.

CC The sequence is that of the whole of rice chloroplast DNA.

```
XX
SQ Sequence 134525 BP; 41249 A; 26129 C; 26331 G; 40816 T; 0 other;
  Query Match          5.6%; Score 33; DB 11; Length 134525;
  Best Local Similarity 100.0%; Pred. No. 1.6e-05;
  Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 149
      |||||
Db 97763 AGCCTGTTATCCCTAGAGTAACCTTTTATCCGTT 97731

RESULT 4
AAC89401/c
ID AAC89401 standard; DNA; 638 BP.
XX
AC AAC89401;
XX
DT 08-MAR-2001 (first entry)
XX
DE E.coli 23S rRNA DNA.
XX
KW 23S rRNA; ribosomal polynucleotide; infection; otitis media;
KW conjunctivitis; pneumonia; bacteremia; meningitis; sinusitis;
KW pleural empyema; endocarditis; ds.
XX
OS Escherichia coli.
XX
PN WO200071560-A1.
XX
PD 30-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-US12133.
XX
PR 20-MAY-1999; 99US-0134973.
PR 07-JUN-1999; 99US-0137837.
PR 14-JUN-1999; 99US-0139095.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Hegg LA, Sterner TA;
XX
WPI; 2001-102280/11.
XX
PT Novel bacterial ribosomal polynucleotides useful for identifying
PT agonists and antagonists for treating otitis media, conjunctivitis,
PT pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
PT endocarditis -
XX
PS Claim 1; Page 16; 67pp; English.
XX
CC The present invention relates to Escherichia coli 23S rRNA.
CC Derivatives from this protein may be useful for treating an
CC individual having a need to inhibit a ribosomal polynucleotide.
CC Agonists and antagonists identified are useful for treating an
CC individual infected by Staphylococcus aureus or Streptococcus
CC pneumoniae. The DNA sequence may also be used in the
CC discovery and screening of antibacterial drugs, and its respective
CC mRNA may be used to construct antisense sequences to control the
CC expression of the coding sequence of interest. The agonists and
CC antagonists are useful for treating otitis media, conjunctivitis,
CC pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
CC endocarditis.
XX
SQ Sequence 638 BP; 149 A; 140 C; 202 G; 147 T; 0 other;
  Query Match          4.5%; Score 27; DB 22; Length 638;
  Best Local Similarity 100.0%; Pred. No. 0.013;
  Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 TAGGAGGAGACCGCCCGCAGTCAAACTA 313
      |||||
Db 287 TAGGAGGAGACCGCCCGCAGTCAAACTA 313

RESULT 5
AAS82419
ID AAS82419 standard; cDNA; 813 BP.
XX
AC AAS82419;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #18223.
XX
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
WPI; 2001-639362/73.
XX
P-PSDB; ABG18232.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 18223; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 813 BP; 200 A; 234 C; 187 G; 192 T; 0 other;
  Query Match          4.5%; Score 27; DB 23; Length 813;
  Best Local Similarity 100.0%; Pred. No. 0.013;
  Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 TAGGAGGAGACCGCCCGCAGTCAAACTA 313
      |||||
Db 411 TAGGAGGAGACCGCCCGCAGTCAAACTA 437
```

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RESULT 6
AAK99200/c
ID AAK99200 standard; RNA; 1258 BP.
XX
AC AAK99200;
XX
DT 11-JUN-2002 (first entry)
XX
DE 1258nt of E-site RNA within E. coli rRNA.
XX
KW RNA-binding; fluorescent reporter molecule; oxazolidinone; viral genome;
KW aminoglycoside; internal ribosome entry site; IRES; E-site RNA; toxic;
KW antibiotic; ss.
XX
OS Escherichia coli.
XX
FH Key Location/Qualifiers
FT misc_binding 2..5
FT /*tag= a
FT /bound_moiety= "Nucleotides 363-360 of itself"
FT /note= "Bound to nucleotides 363-360 of itself"
FT misc_binding 10..17
FT /*tag= b
FT /bound_moiety= "Nucleotides 358-351 of itself"
FT /note= "Bound to nucleotides 358-351 of itself"
FT misc_binding 19..20
FT /*tag= c
FT /bound_moiety= "Nucleotides 349-348 of itself"
FT /note= "Bound to nucleotides 349-348 of itself"
FT stem_loop 36..60
FT /*tag= d
FT stem_loop 62..104
FT /*tag= e
FT misc_binding 106
FT /*tag= f
FT /bound_moiety= "Nucleotide 110 of itself"
FT /note= "Bound to nucleotide 110 of itself"
FT misc_binding 110
FT /*tag= g
FT /bound_moiety= "Nucleotide 106 of itself"
FT /note= "Bound to nucleotide 106 of itself"
FT misc_binding 118..122
FT /*tag= h
FT /bound_moiety= "Nucleotides 342-338 of itself"
FT /note= "Bound to nucleotides 342-338 of itself"
FT misc_binding 125..126
FT /*tag= i
FT /bound_moiety= "Nucleotides 334-333 of itself"
FT /note= "Bound to nucleotides 334-333 of itself"
FT stem_loop 129..143
FT /*tag= j
FT stem_loop 146..181
FT /*tag= k
FT stem_loop 189..259
FT /*tag= l
FT stem_loop 260..278
FT /*tag= m
FT stem_loop 281..298
FT /*tag= n
FT stem_loop 299..315
FT /*tag= o
FT misc_binding 348..349
FT /*tag= p
FT /bound_moiety= "Nucleotides 20-19 of itself"
FT /note= "Bound to nucleotides 20-19 of itself"
FT misc_binding 351..358
FT /*tag= q
FT /bound_moiety= "Nucleotides 17-10 of itself"
FT /note= "Bound to nucleotides 17-10 of itself"
FT misc_binding 360..363
FT /*tag= r
FT /bound_moiety= "Nucleotides 5-2 of itself"

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FT stem_loop /note= "Bound to nucleotides 5-2 of itself"
FT 377..394
FT /*tag= s
FT misc_binding 397..404
FT /*tag= t
FT /bound_moiety= "Nucleotides 979-972 of itself"
FT /note= "Bound to nucleotides 979-972 of itself"
FT misc_binding 406..408
FT /*tag= u
FT /bound_moiety= "Nucleotides 971-969 of itself"
FT /note= "Bound to nucleotides 971-969 of itself"
FT misc_binding 410..411
FT /*tag= v
FT /bound_moiety= "Nucleotides 966-965 of itself"
FT /note= "Bound to nucleotides 966-965 of itself"
FT misc_binding 417..421
FT /*tag= w
FT /bound_moiety= "Nucleotides 801-797 of itself"
FT /note= "Bound to nucleotides 801-797 of itself"
FT misc_binding 423..424
FT /*tag= x
FT /bound_moiety= "Nucleotides 796-795 of itself"
FT /note= "Bound to nucleotides 796-795 of itself"
FT misc_binding 425..429
FT /*tag= y
FT /bound_moiety= "Nucleotides 792-788 of itself"
FT /note= "Bound to nucleotides 792-788 of itself"
FT misc_binding 431..434
FT /*tag= z
FT /bound_moiety= "Nucleotides 597-594 of itself"
FT /note= "Bound to nucleotides 597-594 of itself"
FT misc_binding 438
FT /*tag= aa
FT /bound_moiety= "Nucleotide 589 of itself"
FT /note= "Bound to nucleotide 589 of itself"
FT misc_binding 441..444
FT /*tag= ab
FT /bound_moiety= "Nucleotides 586-583 of itself"
FT /note= "Bound to nucleotides 586-583 of itself"
FT misc_binding 447..452
FT /*tag= ac
FT /bound_moiety= "Nucleotides 550-545 of itself"
FT /note= "Bound to nucleotides 550-545 of itself"
FT misc_binding 455..457
FT /*tag= ad
FT /bound_moiety= "Nucleotides 542-540 of itself"
FT /note= "Bound to nucleotides 542-540 of itself"
FT misc_binding 459..460
FT /*tag= ae
FT /bound_moiety= "Nucleotides 538-537 of itself"
FT /note= "Bound to nucleotides 538-537 of itself"
FT misc_binding 474..478
FT /*tag= af
FT /bound_moiety= "Nucleotides 532-528 of itself"
FT /note= "Bound to nucleotides 532-528 of itself"
FT stem_loop 481..515
FT /*tag= ag
FT misc_binding 528..532
FT /*tag= ah
FT /bound_moiety= "Nucleotides 478-474 of itself"
FT /note= "Bound to nucleotides 478-474 of itself"
FT misc_binding 537..538
FT /*tag= ai
FT /bound_moiety= "Nucleotides 460-459 of itself"
FT /note= "Bound to nucleotides 460-459 of itself"
FT misc_binding 540..542
FT /*tag= aj
FT /bound_moiety= "Nucleotides 457-455 of itself"
FT /note= "Bound to nucleotides 457-455 of itself"
FT misc_binding 545..550
FT /*tag= ak
FT /bound_moiety= "Nucleotides 452-447 of itself"
FT /note= "Bound to nucleotides 452-447 of itself"
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FT stem_loop 554..577
FT /*tag= al
FT 583..586
FT /*tag= am
FT /bound_moiety= "Nucleotides 444-441 of itself"
FT /note= "Bound to nucleotides 444-441 of itself"
FT 589
FT /*tag= an
FT /bound_moiety= "Nucleotide 438 of itself"
FT /note= "Bound to nucleotide 438 of itself"
FT 594..597
FT /*tag= ao
FT /bound_moiety= "Nucleotides 434-431 of itself"
FT /note= "Bound to nucleotides 434-431 of itself"
FT 600..612
FT /*tag= ap
FT 613..635
FT /*tag= aq
FT 642..649
FT /*tag= ar
FT /bound_moiety= "Nucleotides 698-691 of itself"
FT /note= "Bound to nucleotides 698-691 of itself"
FT 650..676
FT /*tag= as
FT 691..698
FT /*tag= at
FT /bound_moiety= "Nucleotides 649-642 of itself"
FT /note= "Bound to nucleotides 649-642 of itself"
FT 701..724
FT /*tag= au
FT 726..735
FT /*tag= av
FT 749..775
FT /*tag= aw
FT 788..792
FT /*tag= ax
FT /bound_moiety= "Nucleotides 434-431 of itself"
FT /note= "Bound to nucleotides 434-431 of itself"
FT 795..796
FT /*tag= ay
FT /bound_moiety= "Nucleotides 424-423 of itself"
FT /note= "Bound to nucleotides 424-423 of itself"
FT 797..801
FT /*tag= az
FT /bound_moiety= "Nucleotides 421-417 of itself"
FT /note= "Bound to nucleotides 421-417 of itself"
FT 809..850
FT /*tag= ba
FT 861
FT /*tag= bb
FT /bound_moiety= "Nucleotide 935 of itself"
FT /note= "Bound to nucleotide 935 of itself"
FT 863..865
FT /*tag= bc
FT /bound_moiety= "Nucleotides 933-931 of itself"
FT /note= "Bound to nucleotides 933-931 of itself"
FT 866

Query Match 4.5%; Score 27; DB 24; Length 1258;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 287 TAGGAGGAGACGCCGCCAGTCAAACTA 313
|||||
Db 620 TAGGAGGAGACGCCGCCAGTCAAACTA 594

RESULT 7
AAS87232/c
ID AAS87232 standard; cDNA; 1446 BP.
XX
AC AAS87232;
XX

FT stem_loop 13-FEB-2002 (first entry)
FT XX
FT DE DNA encoding novel human diagnostic protein #23036.
FT XX
FT KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
FT KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
FT XX
FT OS Homo sapiens.
FT XX
FT PN WO200175067-A2.
FT XX
FT PD 11-OCT-2001.
FT XX
FT PF 30-MAR-2001; 2001WO-US08631.
FT XX
FT PR 31-MAR-2000; 2000US-0540217.
FT PR 23-AUG-2000; 2000US-0649167.
FT XX
FT PA (HYSE-) HYSEQ INC.
FT XX
FT PI Drmanac RT, Liu C, Tang YT;
FT XX
FT DR WPI; 2001-639362/73.
FT DR P-PSDB; ABG23045.
FT XX
FT PT New isolated polynucleotide and encoded polypeptides, useful in
FT PT diagnostics, forensics, gene mapping, identification of mutations
FT PT responsible for genetic disorders or other traits and to assess
FT PT biodiversity.
FT XX
FT PS Claim 1; SEQ ID No 23036; 103pp; English.
FT XX
FT CC The invention relates to isolated polynucleotide (I) and
FT CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
FT CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
FT CC and gene mapping, and in recombinant production of (II). The
FT CC polynucleotides are also used in diagnostics as expressed sequence tags
FT CC for identifying expressed genes. (I) is useful in gene therapy techniques
FT CC to restore normal activity of (II) or to treat disease states involving
FT CC (II). (II) is useful for generating antibodies against it, detecting or
FT CC quantitating a polypeptide in tissue, as molecular weight markers and as
FT CC a food supplement. (II) and its binding partners are useful in medical
FT CC imaging of sites expressing (II). (I) and (II) are useful for treating
FT CC disorders involving aberrant protein expression or biological activity.
FT CC The polypeptide and polynucleotide sequences have applications in
FT CC diagnostics, forensics, gene mapping, identification of mutations
FT CC responsible for genetic disorders or other traits to assess biodiversity
FT CC and to produce other types of data and products dependent on DNA and
FT CC amino acid sequences. AAS64197-AAS94564 represent novel human
FT CC diagnostic coding sequences of the invention.
FT CC Note: The sequence data for this patent did not appear in the printed
FT CC specification, but was obtained in electronic format directly from WIPO
FT CC at ftp.wipo.int/pub/published_pct_sequences.
FT XX
FT SQ Sequence 1446 BP; 331 A; 354 C; 459 G; 302 T; 0 other;

Query Match 4.5%; Score 27; DB 23; Length 1446;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 287 TAGGAGGAGACGCCGCCAGTCAAACTA 313
|||||
Db 815 TAGGAGGAGACGCCGCCAGTCAAACTA 789

RESULT 8
AAS77887/c
ID AAS77887 standard; cDNA; 2115 BP.
XX
AC AAS77887;
XX
DT 13-FEB-2002 (first entry)
XX
```

DE DNA encoding novel human diagnostic protein #13691.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG13700.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity -

XX Claim 1; SEQ ID No 13691; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC; and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human

CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SO Sequence 2115 BP; 389 A; 652 C; 728 G; 346 T; 0 other;

Query Match 4.5%; Score 27; DB 23; Length 2115;

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 TAGGAGGAGACCGCCCGAGTCAAACTA 313

DB 343 TAGGAGGAGACCGCCCGAGTCAAACTA 317

RESULT 9

AAA66047

ID AAA66047 standard; DNA; 2904 BP.

XX AAA66047;

XX 05-OCT-2000 (first entry)

DE E. coli proliferation associated coding sequence SEQ ID NO:239.

XX

KW Escherichia coli; E. coli; proliferation; inhibition; screening;

KW antimicrobial; bacterial growth; antisense therapy; antibacterial; ds.

OS Escherichia coli.

PN WO200044906-A2.

XX 03-AUG-2000.

XX 27-JAN-2000; 2000WO-US02200.

XX 27-JAN-1999; 99US-0117405.

XX (ELIT-) ELITRA PHARM INC.

XX Zyskind J, Ohlsen KL, Trawick J, Forsyth RA, Froelich JM, Carr GJ;

PI Yamamoto RT, Xu HH;

XX WPI; 2000-514822/46.

XX Novel polynucleotides and polypeptides associated with microorganism

PT proliferation, used to identify inhibitors of bacterial growth and

PT proliferation, for use in antisense therapy -

XX Claim 8; Page 172-173; 316pp; English.

XX AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide

CC sequences derived from Escherichia coli which inhibit E. coli

CC proliferation. AAA65890 to AAA66035 and AAB15886 to AAB16040 represent

CC nucleotide and protein sequences associated with E. coli proliferation.

CC AAA66036 and AAA66057 represent primers used for sequencing E. coli

CC proliferation inhibiting nucleotide inserts in an example from the

CC present invention. Methods from the present invention can be used to

CC identify a proliferation- required gene in a microorganism, by contacting

CC a microorganism with a proliferation-required gene activity inhibitory

CC nucleic acid identified in another organism, and determining if

CC inhibition occurs in the second microorganism. The nucleic acid sequences

CC identified as being required for bacterial growth and proliferation, can

CC be used for antisense therapy for killing bacteria.

XX

SO Sequence 2904 BP; 591 A; 912 C; 639 G; 762 T; 0 other;

Query Match 4.5%; Score 27; DB 21; Length 2904;

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 TAGGAGGAGACCGCCCGAGTCAAACTA 313

DB 639 TAGGAGGAGACCGCCCGAGTCAAACTA 665

RESULT 10

AAA66052

ID AAA66052 standard; RNA; 2904 BP.

XX AAA66052;

XX 05-OCT-2000 (first entry)

DE E. coli proliferation associated nucleotide sequence SEQ ID NO:399.

XX

KW Escherichia coli; E. coli; proliferation; inhibition; screening;

KW antimicrobial; bacterial growth; antisense therapy; antibacterial; ss.

OS Escherichia coli.

XX WO200044906-A2.

XX 03-AUG-2000.

XX 27-JAN-2000; 2000WO-US02200.

XX 27-JAN-1999; 99US-0117405.

PR

```

XX (ELIT-) ELITRA PHARM INC.
XX Zyskind J, Ohlsen KL, Trawick J, Forsyth RA, Froelich JM, Carr GJ;
XX Yamamoto RT, Xu HH;
XX WPI; 2000-514822/46.
XX Novel polynucleotides and polypeptides associated with microorganism
XX proliferation, used to identify inhibitors of bacterial growth and
XX proliferation, for use in antisense therapy -
XX
XX Example 3; Page 295-296; 316pp; English.
XX
XX AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide
XX sequences derived from Escherichia coli which inhibit E. coli
XX proliferation. AAA65890 to AAA66055 and AAA65886 to AAA66040 represent
XX nucleotide and protein sequences associated with E. coli proliferation.
XX AAA66056 and AAA66057 represent primers used for sequencing E. coli
XX proliferation inhibiting nucleotide inserts in an example from the
XX present invention. Methods from the present invention can be used to
XX identify a proliferation-required gene in a microorganism, by contacting
XX a microorganism with a proliferation-required gene activity inhibitory
XX nucleic acid identified in another organism, and determining if
XX inhibition occurs in the second microorganism. The nucleic acid sequences
XX identified as being required for bacterial growth and proliferation, can
XX be used for antisense therapy for killing bacteria.
XX
XX Sequence 2904 BP; 591 A; 912 C; 639 G; 762 U; 0 other;
XX
XX Query Match      4.5%; Score 27; DB 21; Length 2904;
XX Best Local Similarity 88.9%; Pred. No. 0.012;
XX Matches 24; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
OY 287 TAGGAGGAGACGCCGCCGTCACAACTA 313
DB 639 UAGGAGGAGACGCCGCCGTCACAACTA 665

RESULT 11
AAH75411/c
ID AAH75411 standard; rRNA; 2904 BP.
XX
XX AC AAH75411;
XX
XX 22-OCT-2001 (first entry)
XX
XX E. coli 23S rRNA.
XX
XX 16S rRNA; 23S rRNA; RNA binding; antimicrobial; ss.
XX
XX Escherichia coli.
XX
XX Key Location/Qualifiers
FH misc_binding 1..8
FT /*tag= a
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 2902-2895 to form a duplex"
FT
FT misc_binding 16..24
FT /*tag= b
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 525-516 to form a duplex"
FT
FT misc_binding 30
FT /*tag= c
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotide 510"
FT
FT misc_binding 31..32
FT /*tag= d
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 474-473 to form a duplex"
FT
FT misc_binding 35..44
FT /*tag= e
FT /bound_moiety= "23S rRNA"

```

```

FT misc_binding
FT /*tag= f
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 116-114 to form a duplex"
FT
FT stem_loop 58..69
FT /*tag= g
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 56-54 to form a duplex"
FT
FT stem_loop 76..110
FT /*tag= h
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 44-35 to form a duplex"
FT
FT misc_binding 114..116
FT /*tag= i
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 268-265 to form a duplex"
FT
FT stem_loop 121..130
FT /*tag= j
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 366-341 to form a duplex"
FT
FT stem_loop 131..148
FT /*tag= k
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 297-271 to form a duplex"
FT
FT stem_loop 150..176
FT /*tag= l
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT stem_loop 184..212
FT /*tag= m
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT stem_loop 224..231
FT /*tag= n
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT stem_loop 235..262
FT /*tag= o
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT misc_binding 265..268
FT /*tag= p
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT misc_binding 271..297
FT /*tag= q
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT stem_loop 301..316
FT /*tag= r
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT stem_loop 319..323
FT /*tag= s
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT stem_loop 325..337
FT /*tag= t
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT misc_binding 341..366
FT /*tag= u
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT stem_loop 376..398
FT /*tag= v
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT stem_loop 406..421
FT /*tag= w
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT misc_binding 424..427
FT /*tag= x
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT misc_binding 433..445
FT /*tag= y
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT stem_loop 461..468
FT /*tag= z
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT misc_binding 473..474
FT /*tag= aa
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT stem_loop 484..496
FT /*tag= ab
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT misc_binding 510
FT /*tag= ac
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotide 30"
FT
FT misc_binding 516..525
FT /*tag= ad
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 24-16 to form a duplex"
FT
FT stem_loop 533..560
FT /*tag= ae

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```
FT misc_binding 579..584
FT /*tag= af
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 1261-1256 to form a duplex"
FT misc_binding 589..601
FT /*tag= ag
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 668-656 to form a duplex"
FT stem_loop 604..624
FT /*tag= ah
FT stem_loop 628..635
FT /*tag= ai
FT stem_loop 638..650
FT /*tag= aj
FT misc_binding 656..668
FT /*tag= ak
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 601-589 to form a duplex"
FT misc_binding 671..672
FT /*tag= al
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 809-808 to form a duplex"
FT misc_binding 678..683
FT /*tag= am
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 799-794 to form a duplex"
FT misc_binding 687..698
FT /*tag= an
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 763-775 to form a duplex"
FT stem_loop 700..732
FT /*tag= ao
FT stem_loop 736..760
FT /*tag= ap
FT protein_bind 752
FT /*tag= aq
FT /bound_moiety= "Vemamycin B"
FT misc_binding 763..775
FT /*tag= ar
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 698-687 to form a duplex"
FT stem_loop 777..787
FT /*tag= as
FT misc_binding 794..799
FT /*tag= at
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 683-678 to form a duplex"
FT misc_binding 808..809
FT /*tag= au
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 672-671 to form a duplex"
FT misc_binding 812..817
FT /*tag= av
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 1195-1190 to form a duplex"
FT stem_loop 822..835
FT /*tag= aw
FT stem_loop 838..940
FT /*tag= ax
FT protein_bind 913
FT /*tag= ay
FT /bound_moiety= "Viomycin"
FT protein_bind 914
FT /*tag= az
FT /bound_moiety= "Viomycin"
FT stem_loop 946..971
FT /*tag= ba
FT stem_loop 976..987
FT /*tag= bb
FT misc_binding 991..998
FT /*tag= bc
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 1163-1157 to form a duplex"
```

```
FT misc_binding 1002..1004
FT /*tag= bd
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 1153-1151 to form a duplex"
FT misc_binding 1011..1019
FT /*tag= be
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 1150-1143 to form a duplex"
FT stem_loop 1030..1043
FT /*tag= bf
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 1124-1112 to form a duplex"
FT misc_feature 1031..1123
FT /*tag= bg
FT /label= "GTPase Centre"
FT misc_binding 1052..1055
FT /*tag= bh
FT /bound_moiety= "23S rRNA"
FT /note= "Binds nucleotides 1107-1104 to form a duplex"
FT stem_loop 1057..1081
FT /*tag= bi
FT protein_bind 1067

Query Match 4.5%; Score 27; DB 22; Length 2904;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 TAGGAGGAGACCGCCCGCAGTCAAACTA 313
DB 2267 TAGGAGGAGACCGCCCGCAGTCAAACTA 2241
|||||
RESULT 12
AAF23016/C
ID AAF23016 standard; rRNA; 2904 BP.
XX AC
XX AAF23016;
XX DT 20-MAR-2001 (first entry)
XX DE E. coli 23S rRNA sequence.
XX KW Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
XX KW Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella;
XX KW Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrhoeae; fungus;
XX KW bacterium; ss.
XX OS Escherichia coli.
XX PN US6150517-A.
XX PD 21-NOV-2000.
XX PF 30-MAY-1995; 95US-0454063.
XX PR 22-FEB-1994; 94US-0200866.
XX PR 24-NOV-1987; 87US-0295208.
XX PR 24-NOV-1987; 87WQ-US03009.
XX PR 11-DEC-1991; 91US-0806929.
XX PR 24-NOV-1986; 86US-0934244.
XX PR 07-AUG-1987; 87US-0083542.
XX (GENP-) GEN-PROBE INC.
XX PI McDonough SH, Kop JA, Smith RD, Hogan JJ;
XX WPI; 2001-060029/07.
XX
XX Preparing a probe for nucleic acid hybridization assays comprises
XX constructing a nucleotide polymer sufficiently complementary to
XX hybridize to an rRNA region that distinguishes non-viral target from
XX non-viral non-target species -
```


PS Disclosure: Fig 2: 75pp; English.

CC The present invention provides novel methods of producing probes for use
 CC in the identification of a number of microorganisms. These include E.
 CC coli, Mycobacteria, Mycoplasma, Campylobacter, Chlamydia, Enterobacter,
 CC Legionella, Salmonella, Pseudomonas, Neisseria gonorrhoeae, fungi and
 CC bacteria.

XX Sequence 2904 BP; 762 A; 639 C; 912 G; 591 U; 0 other;

Query Match 4.5%; Score 27; DB 22; Length 2904;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 TAGGAGGAGACGCCCGCCAGTCAAACTA 313
 |||||
 DB 2266 TAGGAGGAGACGCCCGCCAGTCAAACTA 2240

RESULT 13

AAAC89403/c
 ID AAC89403 standard; DNA; 2904 BP.

XX AAC89403;

DT 08-MAR-2001 (first entry)

DE Sequences from 23S E.coli ribosomal RNA.

KW 23S rRNA; ribosomal polynucleotide; infection; otitis media;
 XW conjunctivitis; pneumonia; bacteremia; meningitis; sinusitis;
 KW pleural empyema; endocarditis; ds.

XX Escherichia coli.

OS WO200071560-A1.

PN 30-NOV-2000.

PD 04-MAY-2000; 2000WO-US12133.

XX 20-MAY-1999; 99US-0134973.

PR 07-JUN-1999; 99US-0137837.

PR 14-JUN-1999; 99US-0139095.

XX (SMK) SMITHKLINE BEECHAM CORP.

PA (SMK) SMITHKLINE BEECHAM PLC.

PI Hegg LA, Sterner TA;

XX WPI; 2001-102280/11.

DR Novel bacterial ribosomal polynucleotides useful for identifying
 XX agonists and antagonists for treating otitis media, conjunctivitis,
 PT pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
 PT endocarditis

PS Claim 10; Page 18-19; 67pp; English.

XX The present invention relates to Escherichia coli 23S rRNA.

CC Derivatives from this protein may be useful for treating an
 CC individual having a need to inhibit a ribosomal polynucleotide.
 CC Agonists and antagonists identified are useful for treating an
 CC individual infected by Staphylococcus aureus or Streptococcus
 CC pneumoniae. The DNA sequence may also be used in the

CC discovery and screening of antibacterial drugs, and its respective
 CC mRNA may be used to construct antisense sequences to control the
 CC expression of the coding sequence of interest. The agonists and
 CC antagonists are useful for treating otitis media, conjunctivitis,
 CC pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
 CC endocarditis.

XX Sequence 2904 BP; 762 A; 639 C; 912 G; 591 T; 0 other;

Query Match

Best Local Similarity 4.5%; Score 27; DB 22; Length 2904;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 TAGGAGGAGACGCCCGCCAGTCAAACTA 313
 |||||
 DB 2266 TAGGAGGAGACGCCCGCCAGTCAAACTA 2240

RESULT 14

AAV38096/c

ID AAV38096 standard; DNA; 2907 BP.

XX AAV38096;

DT 15-SEP-1998 (first entry)

DE Enterohaemorrhagic E. coli 0157 23A rRNA gene DNA sequence.

KW Enterohaemorrhagic; Escherichia coli 0157; 23S rRNA; hybridisation;
 KW probe; detection; diagnosis; infection; PCR primer; ds.

XX Escherichia coli.

OS JP10165182-A.

PN 23-JUN-1998.

XX 09-DEC-1996; 96JP-0328837.

PR 09-DEC-1996; 96JP-0328837.

XX (NIFL-) NIPPON FLOUR MILLS CO LTD.

PA (ZENK-) ZENKOKU NOGYO KYODO KUMIAI RENGOKAI.

XX WPI; 1998-416777/36.

XX Hybridisation probe derived from 23S ribosomal RNA of

PT enterohaemorrhagic E. coli 0157 - or the gene encoding the 23S
 PT ribosomal RNA; used for the specific detection of enterohaemorrhagic
 PT E. coli 0157

XX Example 2; Page 5-6; 18pp; Japanese.

XX A method has been developed for the detection of enterohaemorrhagic
 CC Escherichia coli (EHEC) 0157 in which nucleic acid fragments of the
 CC 23S ribosomal RNA (rRNA) gene from EHEC 0157 are used as hybridisation
 CC probes. The present sequence represents the 23S rRNA gene from EHEC 0157
 CC from the present invention. Probes from the present invention can be
 CC labelled and used as hybridisation probes to detect EHEC 0157 in a
 CC sample. They can specifically detect E. coli 0157 and hence diagnose
 CC infection.

XX Sequence 2907 BP; 760 A; 638 C; 909 G; 592 T; 8 other;

Query Match

Best Local Similarity 4.5%; Score 27; DB 19; Length 2907;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 287 TAGGAGGAGACGCCCGCCAGTCAAACTA 313
 |||||
 DB 2269 TAGGAGGAGACGCCCGCCAGTCAAACTA 2243

RESULT 15

AAV38107/c

ID AAV38107 standard; rRNA; 2907 BP.

XX AAV38107;

DT 15-SEP-1998 (first entry)

```

DE Enterohaemorrhagic E. coli 0157 23A rRNA gene rRNA sequence.
XX
KW Enterohaemorrhagic; Escherichia coli 0157; 23S rRNA; hybridisation;
KW probe; detection; diagnosis; infection; PCR primer; ss.
XX
OS Escherichia coli.
XX
PN JPL10165182-A.
XX
XX 23-JUN-1998.
XX
XX
PF 09-DEC-1996; 96JP-0328837.
XX
XX 09-DEC-1996; 96JP-0328837.
XX
PA (NIFL-) NIPPON FLOUR MILLS CO LTD.
PA (ZENK-) ZENKOKU NOGYO KYODO KUMIAI RENGOKAI.
XX
DR WPI; 1998-416777/36.
XX
XX Hybridisation probe derived from 23S ribosomal RNA of
PT enterohaemorrhagic E. coli 0157 - or the gene encoding the 23S
PT ribosomal RNA; used for the specific detection of enterohaemorrhagic
PT E. coli 0157
XX
PS Disclosure; Page 4-5; 18pp; Japanese.
XX
XX A method has been developed for the detection of enterohaemorrhagic
CC Escherichia coli (EHEC) 0157 in which nucleic acid fragments of the
CC 23S ribosomal RNA (rRNA) gene from EHEC 0157 are used as hybridisation
CC probes. The present sequence represents the 23S rRNA gene from EHEC 0157
CC from the present invention. Probes from the present invention can be
CC labelled and used as hybridisation probes to detect EHEC 0157 in a
CC sample. They can specifically detect E. coli 0157 and hence diagnose
CC infection.
XX
XX Sequence 2907 BP; 760 A; 638 C; 909 G; 592 U; 8 other;
SQ
Query Match 4.5%; Score 27; DB 19; Length 2907;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 287 TAGGAGGAGACCGCCCGCAGTCAAACTA 313
Db 2269 TAGGAGGAGACCGCCCGCAGTCAAACTA 2243
Search completed: December 11, 2002, 20:39:05
Job time : 421 secs

```

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 19:18:03 ; Search time 3172 Seconds
(without alignments)
5449.895 Million cell updates/sec

Title: US-09-369-992c-l_COPY_1147_1740

Perfect score: 594

Sequence: 1 gtagcgtttaatagcgaa.....ttacatctttcatgcaggtc 594

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

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6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

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32: em_hgt_other.*

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34: em_hgt_pln.*

35: em_hgt_rod.*

36: em_hgt_mam.*

37: em_hgt_vrt.*

38: em_sv.*

39: em_hgt_hum.*

40: em_hgt_mus.*

41: em_hgt_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	594	100.0	5849	3	PB079731	U79731 Plasmodium
2	497	83.7	2621	3	PB079732	U79732 Plasmodium
3	237	39.9	594	3	AF182847	AF182847 Plasmodium
c 4	123	20.7	594	3	PM097565	PM097565 Plasmodium
c 5	123	20.7	594	3	PM097561	PM097561 Plasmodium
c 6	123	20.7	594	3	PM097562	PM097562 Plasmodium
c 7	117	19.7	594	3	PM097559	PM097559 Plasmodium
c 8	117	19.7	594	3	PM097557	PM097557 Plasmodium
c 9	117	19.7	594	3	PM097558	PM097558 Plasmodium
c 10	117	19.7	594	3	PM097560	PM097560 Plasmodium
c 11	117	19.7	594	3	PM097563	PM097563 Plasmodium
c 12	117	19.7	594	3	PM097564	PM097564 Plasmodium
c 13	117	19.7	594	3	PM097556	PM097556 Plasmodium
c 14	117	19.7	2700	3	PF182846	PF182846 Plasmodium
c 15	117	19.7	5142	3	PF182846	PF182846 Plasmodium
c 16	117	19.7	15421	3	PF182846	PF182846 Plasmodium
c 17	66	11.1	594	3	PF182846	PF182846 Plasmodium
c 18	39	6.6	2700	3	PF182846	PF182846 Plasmodium
c 19	39	6.6	3269	3	PF182846	PF182846 Plasmodium
c 20	39	6.6	4859	8	PF182846	PF182846 Plasmodium
c 21	39	6.6	6113	3	PF182846	PF182846 Plasmodium
c 22	39	6.6	7847	3	PF182846	PF182846 Plasmodium
c 23	39	6.6	34996	3	PF182846	PF182846 Plasmodium
c 24	39	6.6	34996	3	PF182846	PF182846 Plasmodium
c 25	38	6.4	2558	8	PF182846	PF182846 Plasmodium
c 26	35	5.9	2840	8	PF182846	PF182846 Plasmodium
c 27	33	5.6	117	8	PF182846	PF182846 Plasmodium
c 28	33	5.6	238	8	PF182846	PF182846 Plasmodium
c 29	33	5.6	664	8	PF182846	PF182846 Plasmodium
c 30	33	5.6	675	8	PF182846	PF182846 Plasmodium
c 31	33	5.6	955	8	PF182846	PF182846 Plasmodium
c 32	33	5.6	957	8	PF182846	PF182846 Plasmodium
c 33	33	5.6	1064	8	PF182846	PF182846 Plasmodium
c 34	33	5.6	1080	8	PF182846	PF182846 Plasmodium
c 35	33	5.6	1130	8	PF182846	PF182846 Plasmodium
c 36	33	5.6	1986	8	PF182846	PF182846 Plasmodium
c 37	33	5.6	2524	8	PF182846	PF182846 Plasmodium
c 38	33	5.6	2552	8	PF182846	PF182846 Plasmodium
c 39	33	5.6	2568	8	PF182846	PF182846 Plasmodium
c 40	33	5.6	2571	8	PF182846	PF182846 Plasmodium
c 41	33	5.6	2571	8	PF182846	PF182846 Plasmodium
c 42	33	5.6	2572	8	PF182846	PF182846 Plasmodium
c 43	33	5.6	2603	8	PF182846	PF182846 Plasmodium
c 44	33	5.6	2610	8	PF182846	PF182846 Plasmodium
c 45	33	5.6	2619	8	PF182846	PF182846 Plasmodium

ALIGNMENTS

RESULT 1
PB079731

LOCUS
DEFINITION

PB079731 5849 bp DNA linear INV 05-DEC-1997
Plasmodium berghei extrachromosomal plasmid PB-1. ORF470 gene,
partial cds, tRNA-Thr, large subunit ribosomal RNA, tRNA-Met,
tRNA-Arg, tRNA-Val, tRNA-Leu, tRNA-Asn, tRNA-Ala, and
small subunit ribosomal RNA genes, complete sequences.

U79731 GI:2662401

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Plasmodium berghei.
Plasmodium berghei
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 5849)
Yap,M.W., Kara,U.A., ten Heggeler-Bordier,B., Ting,R.C. and

Tan,T.M.
Partial nucleotide sequence and organisation of extrachromosomal
plastid-like DNA in Plasmodium berghei

Gene 200 (1-2), 91-98 (1997)

89038979

9373142

2 (bases 1 to 5849)

Yap,M.W.C., Kara,U.A.K. and Tan,T.M.C.

Direct Submission

Submitted (26-NOV-1996) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore

Location/Qualifiers

1. 5849

/organism="Plasmodium berghei"

/strain="ANKA"

/db_xref="taxon:5821"

/note="extrachromosomal plastid PB-1"

complement(<1..711)

/note="ORF470"

/codon_start=1

/protein_id="AAB88271.1"

/db_xref="GI:2662403"

/translation="MINKLKLKFLNLYNLYQYNNKINLYLRNGLNKNLIKNS
NNIYLFYFKIYSLKFLNMFKLPDMSCEPNISYDNIYYSSTLKDSNLVLYK
TNLINFIDTYFNKIIPIIDVICDSISVLHTQYFLKGLGIIFLSLIDVILKYPPLVK
KVLGTVVSYKDNFPANINSIIFSGSFYVSKYIKCSFNLSTVFETKINSYDFAQFRTL
LIASEFAYGVLEGCTASL"

complement(739..809)

/product="rRNA-Thr"

complement(814..3521)

/product="large subunit ribosomal RNA"

complement(3565..3636)

/product="rRNA-Met"

complement(3646..3717)

/product="rRNA-Arg"

3742..3813

/product="rRNA-Val"

3817..3888

/product="rRNA-Arg"

3895..3975

/product="rRNA-Leu"

complement(3996..4058)

/product="rRNA-Asn"

4089..4159

/product="rRNA-Ala"

4208..5648

/product="small subunit ribosomal RNA"

5793..5849

/product="rRNA-Ile"

BASE COUNT 2296 a 673 c 557 g 2323 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.8e-284;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCGCTTATAGCGCAAGACTTACCTTAAACATACACTACTGCTTAGGATCGGA 60
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Db 1147 GATCGCTTATAGCGCAAGACTTACCTTAAACATACACTACTGCTTAGGATCGGA 1206
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QY 61 TAAGCGGACATCGAGTGCCAAACCTTTTCGTCATATGGACTCTCGGAAAGATTAGCC 120
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Db 1207 TAAGCGGACATCGAGTGCCAAACCTTTTCGTCATATGGACTCTCGGAAAGATTAGCC 1266
|||||

QY 121 TGTATCCCTAGAGTAACCTTTATCCGTTAAGCGGATAATTTATATTAATAAATATCG 180
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Db 1267 TGTATCCCTAGAGTAACCTTTATCCGTTAAGCGGATAATTTATATTAATAAATATCG 1326
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QY 181 GATCATTAGCCGACATTAATCTCTGTTAATTTGTTAAATTTTACAGTTAATATATAT 240
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Db 1327 GATCATTAGCCGACATTAATCTCTGTTAATTTGTTAAATTTTACAGTTAATATATAT 1386
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QY 241 TTATCTTTTATATAATAATAACATTTGACACCTCCGTTTTTATATAGGAGGACCGC 300
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Db 1387 TTATCTTTTATATAATAATAACATTTGACACCTCCGTTTTTATATAGGAGGACCGC 1446
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QY 301 CCCAGTCAACATCTCTTATAAATATTTGTTAAATAATTTTGTATATAAATAATTTATAGAAAT 360
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Db 1447 CCCAGTCAACATCTCTTATAAATATTTGTTAAATAATTTTGTATATAAATAATTTATAGAAAT 1506
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QY 361 TTATATATATAAATAAGGTATTTCAATTAACAATTTACATATTTCCAAAAAATAATATT 420
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Db 1507 TTATATATATAAATAAGGTATTTCAATTAACAATTTACATATTTCCAAAAAATAATATT 1566
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QY 421 ACTACTTCCCATTATCTATCTATATATATATATATATATTTTCAATATCTATATAGTAAG 480
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Db 1567 ACTACTTCCCATTATCTATCTATATATATATATATATTTTCAATATCTATATAGTAAG 1626
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QY 481 CTTCATAGGGTCTTTCTGCTCCTAATAATAAGAATCTGCATCTTCACAGATAATTTTATTT 540
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Db 1627 CTTCATAGGGTCTTTCTGCTCCTAATAATAAGAATCTGCATCTTCACAGATAATTTTATTT 1686
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QY 541 CATTAAGATTTTTTTTAAAGCAGCATTTTAAAGTCGTTACATCTTTTCATCGAGTC 594
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Db 1687 CATTAAGATTTTTTTTAAAGCAGCATTTTAAAGTCGTTACATCTTTTCATCGAGTC 1740
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RESULT 2

PBU79732

LOCUS

DEFINITION

PBU79732 2621 bp DNA linear INV 05-DEC-1997

Plasmodium berghei extrachromosomal plastid PB-2, rRNA-Pro,
rRNA-Glu, rRNA-Lys, rRNA-Asp, rRNA-Ser, rRNA-Tyr, rRNA-Met,
rRNA-Leu, rRNA-Cys, and rRNA-His genes, complete sequence, rps4
gene, complete cds, rRNA-Thr gene, complete sequence, and large
subunit ribosomal RNA gene, partial sequence.

U79732

U79732.1 GI:2662403

Plasmodium berghei.

Plasmodium berghei

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE

1 (bases 1 to 2621)

Yap,M.W., Kara,U.A., ten Heggeler-Bordier,B., Ting,R.C. and
Tan,T.M.

PARTIAL nucleotide sequence and organisation of extrachromosomal
plastid-like DNA in Plasmodium berghei

Gene 200 (1-2), 91-98 (1997)

89038979

9373142

2 (bases 1 to 2621)

Yap,M.W.C., Kara,U.A.K. and Tan,T.M.C.

Direct Submission

Submitted (26-NOV-1996) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore

Location/Qualifiers

1. 2621

/organism="Plasmodium berghei"

/strain="ANKA"

/db_xref="taxon:5821"

/note="extrachromosomal plastid PB-2"

complement(2..73)

/product="rRNA-Pro"

complement(91..160)

/product="rRNA-Glu"

complement(172..240)

/product="rRNA-Lys"

complement(250..324)

/product="rRNA-Asp"

complement(336..422)

/product="rRNA-Ser"

complement(432..516)

/product="rRNA-Tyr"

complement(521..607)

/product="rRNA-Met"

FEATURES

source

trna

trna

trna

trna

trna

trna

trna


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/organism="Plasmodium malariae"
/isolate="primary isolate pv16/1"
/db_xref="taxon:5858"
/notes="extrachromosomal plastid"
<1..>593
/product="large subunit ribosomal RNA"
227 a 70 c 98 g 198 t

BASE COUNT
ORIGIN

Query Match 20.7%; Score 123; DB 3; Length 593;
Best Local Similarity 100.0%; Pred. No. 3.7e-50;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 472 ATAGTAAAGCTTCATAGGGCTTTCTGCTCAATATAGAATCTGCATCTTCACAGATA 531
Db 123 ATAGTAAAGCTTCATAGGGCTTTCTGCTCAATATAGAATCTGCATCTTCACAGATA 64

QY 532 ATTTTATTCATTAGATTTTTTTTAAGACAGCATTTAAGTCGTATACATCTTTCATGCAG 591
Db 63 ATTTTATTCATTAGATTTTTTTTAAGACAGCATTTAAGTCGTATACATCTTTCATGCAG 4

QY 592 GTC 594
Db 3 GTC 1

RESULT 5
PVU97561/c
LOCUS
DEFINITION Plasmodium vivax extrachromosomal plastid large subunit ribosomal
RNA gene, partial sequence.
ACCESSION U97561
VERSION U97561.1 GI:4100399
KEYWORDS
SOURCE Plasmodium vivax.
ORGANISM Plasmodium vivax
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 594)
AUTHORS Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
TITLE Direct PCR amplification and sequence analysis of extrachromosomal
Plasmodium DNA from dried blood spots
JOURNAL Acta Trop. 68 (1), 105-114 (1997)
MEDLINE 98013247
PUBMED 9352006
REFERENCE 2 (bases 1 to 594)
AUTHORS Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore
FEATURES
Source
1..594
/organism="Plasmodium vivax"
/isolate="primary isolate pv13/p"
/db_xref="taxon:5855"
/notes="extrachromosomal plastid"
<1..>594
/product="large subunit ribosomal RNA"
225 a 72 c 99 g 198 t

BASE COUNT
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.7e-50;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 472 ATAGTAAAGCTTCATAGGGCTTTCTGCTCAATATAGAATCTGCATCTTCACAGATA 531
Db 123 ATAGTAAAGCTTCATAGGGCTTTCTGCTCAATATAGAATCTGCATCTTCACAGATA 64

QY 532 ATTTTATTCATTAGATTTTTTTTAAGACAGCATTTAAGTCGTATACATCTTTCATGCAG 591
Db 63 ATTTTATTCATTAGATTTTTTTTAAGACAGCATTTAAGTCGTATACATCTTTCATGCAG 4

QY 592 GTC 594
Db 3 GTC 1

RESULT 7
PFU97559/c
LOCUS
DEFINITION Plasmodium falciparum extrachromosomal plastid large subunit
ribosomal RNA gene, partial sequence.
ACCESSION U97559
VERSION U97559.1 GI:4100397
KEYWORDS
SOURCE Plasmodium falciparum.
ORGANISM Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 594)
AUTHORS Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
TITLE Direct PCR amplification and sequence analysis of extrachromosomal
Plasmodium DNA from dried blood spots
JOURNAL Acta Trop. 68 (1), 105-114 (1997)

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QY 592 GTC 594
Db 3 GTC 1

RESULT 6
PVU97562/c
LOCUS
DEFINITION Plasmodium vivax extrachromosomal plastid large subunit ribosomal
RNA gene, partial sequence.
ACCESSION U97562
VERSION U97562.1 GI:4100400
KEYWORDS
SOURCE Plasmodium vivax.
ORGANISM Plasmodium vivax
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 594)
AUTHORS Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
TITLE Direct PCR amplification and sequence analysis of extrachromosomal
Plasmodium DNA from dried blood spots
JOURNAL Acta Trop. 68 (1), 105-114 (1997)
MEDLINE 98013247
PUBMED 9352006
REFERENCE 2 (bases 1 to 594)
AUTHORS Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore
FEATURES
Source
1..594
/organism="Plasmodium vivax"
/isolate="primary isolate pv13/p"
/db_xref="taxon:5855"
/notes="extrachromosomal plastid"
<1..>594
/product="large subunit ribosomal RNA"
225 a 72 c 99 g 198 t

BASE COUNT
ORIGIN

Query Match 20.7%; Score 123; DB 3; Length 594;
Best Local Similarity 100.0%; Pred. No. 3.7e-50;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 472 ATAGTAAAGCTTCATAGGGCTTTCTGCTCAATATAGAATCTGCATCTTCACAGATA 531
Db 123 ATAGTAAAGCTTCATAGGGCTTTCTGCTCAATATAGAATCTGCATCTTCACAGATA 64

QY 532 ATTTTATTCATTAGATTTTTTTTAAGACAGCATTTAAGTCGTATACATCTTTCATGCAG 591
Db 63 ATTTTATTCATTAGATTTTTTTTAAGACAGCATTTAAGTCGTATACATCTTTCATGCAG 4

QY 592 GTC 594
Db 3 GTC 1

RESULT 7
PFU97559/c
LOCUS
DEFINITION Plasmodium falciparum extrachromosomal plastid large subunit
ribosomal RNA gene, partial sequence.
ACCESSION U97559
VERSION U97559.1 GI:4100397
KEYWORDS
SOURCE Plasmodium falciparum.
ORGANISM Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 594)
AUTHORS Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
TITLE Direct PCR amplification and sequence analysis of extrachromosomal
Plasmodium DNA from dried blood spots
JOURNAL Acta Trop. 68 (1), 105-114 (1997)

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MEDLINE
 PUBMED
 REFERENCE
 2 (bases 1 to 594)
 Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
 Direct Submission
 Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
 National University of Singapore, 10 Kent Ridge Crescent S119260,
 Singapore

FEATURES
 source
 1. .594
 /organism="Plasmodium falciparum"
 /isolate="primary isolate pf20/1"
 /db_xref="taxon:5833"
 /note="extrachromosomal plasmid"
 <1. .>594
 /product="large-subunit ribosomal RNA"
 BASE COUNT 231 a 71 c 90 g 202 t
 ORIGIN

Query Match 19.7%; Score 117; DB 3; Length 594;
 Best Local Similarity 100.0%; Pred. No. 3.6e-47;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TTAGATGCGATAGCGACATCGAGTGGCGCAACCTTTTCGTCAATATGGACTCTCGGA 109
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 Db 545 TTAGATGCGATAGCGACATCGAGTGGCGCAACCTTTTCGTCAATATGGACTCTCGGA 486
 |||||
 QY 110 AAAGATTAGCCTGTTATCCCTAGTAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 166
 |||||
 pb 485 AAAGATTAGCCTGTTATCCCTAGTAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 429
 |||||

RESULT 8
 PFU97557/c
 FOCUS
 DEFINITION
 Plasmodium falciparum extrachromosomal plasmid large subunit
 ribosomal RNA gene, partial sequence.
 VERSION
 097557
 KEYWORDS
 097557.1 GI:4100395
 SOURCE
 Plasmodium falciparum.
 ORGANISM
 Plasmodium falciparum
 Plasmodium falciparum
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 1 (bases 1 to 595)
 Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
 Direct PCR amplification and sequence analysis of extrachromosomal
 Plasmidium DNA from dried blood spots
 Acta Trop. 68 (1), 105-114 (1997)
 JOURNAL
 MEDLINE
 98013247
 PUBMED
 9352006
 2 (bases 1 to 595)
 Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
 Direct Submission
 Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
 National University of Singapore, 10 Kent Ridge Crescent S119260,
 Singapore

FEATURES
 source
 1. .595
 /organism="plasmodium falciparum"
 /isolate="primary isolate pf1/p"
 /db_xref="taxon:5833"
 /note="extrachromosomal plasmid"
 <1. .>595
 /product="large subunit ribosomal RNA"
 BASE COUNT 229 a 77 c 93 g 196 t
 ORIGIN

Query Match 19.7%; Score 117; DB 3; Length 595;
 Best Local Similarity 100.0%; Pred. No. 3.6e-47;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TTAGATGCGATAGCGACATCGAGTGGCGCAACCTTTTCGTCAATATGGACTCTCGGA 109
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 Db 545 TTAGATGCGATAGCGACATCGAGTGGCGCAACCTTTTCGTCAATATGGACTCTCGGA 486
 |||||
 QY 110 AAAGATTAGCCTGTTATCCCTAGTAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 166
 |||||
 pb 485 AAAGATTAGCCTGTTATCCCTAGTAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 429
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Db	546	TTAGATCGGATAGACCGACATCGAGGTGCGCAAAACCTTTTCGTCAATATGACTCTCGGA	487
Qy	110	AAAGATTAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTA	166
Db	486	AAAGATTAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTA	430
RESULT 9			
PFU97558/c			
LOCUS			
DEFINITION	PFU97558	595 bp DNA linear	INV 15-MAR-2001
ACCESSION	Plasmodium falciparum extrachromosomal plastid large subunit		
VERSION	ribosomal RNA gene, partial sequence.		
KEYWORDS	U97558		
SOURCE	U97558.1	GI:4100396	
ORGANISM	Plasmodium falciparum.		
REFERENCE	Plasmodium falciparum		
AUTHORS	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
TITLE	1 (bases 1 to 595)		
JOURNAL	Tan, T.M., Nelson, J.S., Ng, H.C., Ting, R.C. and Kara, U.A.		
MEDLINE	Direct PCR amplification and sequence analysis of extrachromosomal		
PUBMED	Plasmodium DNA from dried blood spots		
REFERENCE	Acta Trop. 68 (1), 105-114 (1997)		
AUTHORS	98013247		
TITLE	2 (bases 1 to 595)		
JOURNAL	Tan, T.M.C., Nelson, J.S., Ng, H.C., Ting, R.C.Y. and Kara, U.A.K.		
MEDLINE	Direct Submission		
PUBMED	Submitted (15-APR-1997) Institute of Molecular and Cell Biology,		
REFERENCE	National University of Singapore, 10 Kent Ridge Crescent S119260,		
AUTHORS	Singapore		
TITLE	Location/Qualifiers		
JOURNAL	1. .595		
MEDLINE	/organism="Plasmodium falciparum"		
PUBMED	/isolate="primary isolate pf19/i"		
REFERENCE	/db.xref="taxon:5833"		
AUTHORS	/note="extrachromosomal plastid"		
TITLE	<1. .>595		
JOURNAL	/product="large subunit ribosomal RNA"		
MEDLINE	BASE COUNT 233 a 72 c 89 g 201 t		
PUBMED	ORIGIN		
Query Match	19.78; Score 117; DB 3; Length 595;		
Best Local Similarity	100.0%; Pred. No. 3.6e-47;		
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	50	TTAGATCGGATAGACCGACATCGAGGTGCGCAAAACCTTTTCGTCAATATGACTCTCGGA	109
Db	546	TTAGATCGGATAGACCGACATCGAGGTGCGCAAAACCTTTTCGTCAATATGACTCTCGGA	487
Qy	110	AAAGATTAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTA	166
Db	486	AAAGATTAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTA	430
RESULT 10			
PFU97560/c			
LOCUS			
DEFINITION	PFU97560	595 bp DNA linear	INV 15-MAR-2001
ACCESSION	Plasmodium falciparum extrachromosomal plastid large subunit		
VERSION	ribosomal RNA gene, partial sequence.		
KEYWORDS	U97560		
SOURCE	U97560.1	GI:4100398	
ORGANISM	Plasmodium falciparum.		
REFERENCE	Plasmodium falciparum		
AUTHORS	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
TITLE	1 (bases 1 to 595)		
JOURNAL	Tan, T.M., Nelson, J.S., Ng, H.C., Ting, R.C. and Kara, U.A.		
MEDLINE	Direct PCR amplification and sequence analysis of extrachromosomal		
PUBMED	Plasmodium DNA from dried blood spots		
REFERENCE	Acta Trop. 68 (1), 105-114 (1997)		
AUTHORS	98013247		
TITLE	2 (bases 1 to 595)		
JOURNAL	Tan, T.M.C., Nelson, J.S., Ng, H.C., Ting, R.C.Y. and Kara, U.A.K.		
MEDLINE	Direct Submission		
PUBMED	Submitted (15-APR-1997) Institute of Molecular and Cell Biology,		
REFERENCE	National University of Singapore, 10 Kent Ridge Crescent S119260,		
AUTHORS	Singapore		
TITLE	Location/Qualifiers		
JOURNAL	1. .595		
MEDLINE	/organism="Plasmodium falciparum"		
PUBMED	/isolate="primary isolate pf19/i"		
REFERENCE	/db.xref="taxon:5833"		
AUTHORS	/note="extrachromosomal plastid"		
TITLE	<1. .>595		
JOURNAL	/product="large subunit ribosomal RNA"		
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PUBMED	ORIGIN		
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Best Local Similarity	100.0%; Pred. No. 3.6e-47;		
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

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REFERENCE 2 (bases 1 to 595)
AUTHORS Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1997) Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent S119260, Singapore

FEATURES             Location/Qualifiers
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Db 546 TTAGATCGGATAGCCGACATCGAGTGCCAAACCTTTTCGTCATATGGACTCTCGGA 487
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Qy 110 AAAGATTAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTA 166
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RESULT 11
PVU97563/c
LOCUS                596 bp   DNA   linear   INV 15-MAR-2001
DEFINITION           Plasmodium vivax extrachromosomal plastid large subunit ribosomal
                    RNA gene, partial sequence.
ACCESSION             U97563
VERSION               U97563.1
KEYWORDS              GI:4100401
SOURCE                Plasmodium vivax.
ORGANISM              Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE             1 (bases 1 to 596)
AUTHORS              Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
TITLE                Direct PCR amplification and sequence analysis of extrachromosomal
                    Plasmodium DNA from dried blood spots
JOURNAL              Acta Trop. 68 (1), 105-114 (1997)
MEDLINE              98013247
PUBMED               9352006
REFERENCE             2 (bases 1 to 596)
AUTHORS              Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE                Direct Submission
JOURNAL              Submitted (15-APR-1997) Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent S119260, Singapore

FEATURES             Location/Qualifiers
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RESULT 13
PVU97556/c
LOCUS                598 bp   DNA   linear   INV 15-MAR-2001
DEFINITION           Plasmodium falciparum extrachromosomal plastid large subunit
                    ribosomal RNA gene, partial sequence.
ACCESSION             U97556
VERSION               U97556.1
KEYWORDS              GI:4100394
SOURCE                Plasmodium falciparum.
ORGANISM              Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE             1 (bases 1 to 598)
AUTHORS              Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
TITLE                Direct PCR amplification and sequence analysis of extrachromosomal
                    Plasmodium DNA from dried blood spots
JOURNAL              Acta Trop. 68 (1), 105-114 (1997)
MEDLINE              98013247
PUBMED               9352006
REFERENCE             2 (bases 1 to 598)
AUTHORS              Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.

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DEFINITION           Plasmodium vivax extrachromosomal plastid large subunit ribosomal
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ACCESSION             U97564
VERSION               U97564.1
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SOURCE                Plasmodium vivax.
ORGANISM              Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE             1 (bases 1 to 596)
AUTHORS              Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
TITLE                Direct PCR amplification and sequence analysis of extrachromosomal
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JOURNAL              Acta Trop. 68 (1), 105-114 (1997)
MEDLINE              98013247
PUBMED               9352006
REFERENCE             2 (bases 1 to 596)
AUTHORS              Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
TITLE                Direct Submission
JOURNAL              Submitted (15-APR-1997) Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent S119260, Singapore

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RESULT 13
PVU97556/c
LOCUS                598 bp   DNA   linear   INV 15-MAR-2001
DEFINITION           Plasmodium falciparum extrachromosomal plastid large subunit
                    ribosomal RNA gene, partial sequence.
ACCESSION             U97556
VERSION               U97556.1
KEYWORDS              GI:4100394
SOURCE                Plasmodium falciparum.
ORGANISM              Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE             1 (bases 1 to 598)
AUTHORS              Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
TITLE                Direct PCR amplification and sequence analysis of extrachromosomal
                    Plasmodium DNA from dried blood spots
JOURNAL              Acta Trop. 68 (1), 105-114 (1997)
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AUTHORS              Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.

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TITLE Direct Submission
JOURNAL Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
National University of Singapore, 10 Kent Ridge Crescent S119260,
Singapore

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LOCUS 2700 bp DNA linear INV 27-SEP-1995
DEFINITION Plasmodium falciparum gene for a large subunit ribosomal RNA from
the inverted repeat within the 35-kb circular DNA.
ACCESSION X61660
VERSION 1
KEYWORDS ribosomal RNA; ribosomal RNA large subunit.
SOURCE Plasmodium falciparum
ORGANISM Plasmodium falciparum
REFERENCE 1 (bases 1 to 2700)
AUTHORS Gardner,M.J.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-1991) M.J. Gardner, Div of Parasitology, National
Inst for Medical Research, The Ridgeway - Mill Hill, London NW7
1AA, UK

REFERENCE 2 (bases 1 to 2700)
AUTHORS Gardner,M.J., Feagin,J.E., Moore,D.J., Rangachari,K.,
Williamson,D.H. and Wilson,R.J.
TITLE Sequence and organization of large subunit rRNA genes from the
extrachromosomal 35 kb circular DNA of the malaria parasite
Plasmodium falciparum
JOURNAL Nucleic Acids Res. 21 (5), 1067-1071 (1993)
MEDLINE 93219063
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Db 2267 AAGATTAGCCTGTATCCCTAGAGTAACCTTTATCCGTTAAGCGATAATTTTATTA 2211
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ACCESSION X75545
VERSION 1
KEYWORDS large ribosomal subunit; small ribosomal subunit RNA; transfer
RNA-Ala; transfer RNA-Arg; transfer RNA-Asn; transfer RNA-Ile;
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trnI gene; trnL gene; trnM gene; trnN gene; trnR gene; trnT gene;
trnV gene.

SOURCE Plasmodium falciparum.
ORGANISM Plasmodium falciparum
REFERENCE 1 (bases 1 to 5142)
AUTHORS Gardner,M., Preiser,P., Rangachari,K., Moore,D., Feagin,D.,
Williamson,D.H. and Wilson,R.J.
TITLE Nine duplicated tRNA genes on the plastid-like DNA of the malaria
parasite Plasmodium falciparum
JOURNAL Gene 140, 307-308 (1994)
REFERENCE 2 (bases 1 to 5142)
AUTHORS Wilson,R.J.M.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1993) R.J.M. Wilson, National Institute for
Medical Research, Mill Hill, London NW7 1AA, UK

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Db 4596 AAAGATTAGCCTGTTATCCCTAGAGTAACCTTTTATCCGTTAAGCGATAATTTTATTA 4540
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Nucleic Acids Research, Vol 23, Issue 21 4329-4336,
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[Preiser, P.](#) || [Wilson, R. J.](#)
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[new articles cite this article](#)
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tRNA genes transcribed from the plastid-like DNA of Plasmodium falciparum

P Preiser, DH Williamson and RJ Wilson

Division of Parasitology, National Institute for Medical Research, Mill Hill, London, UK.

Besides their mitochondrial genome, malarial parasites contain a second organellar DNA. This 35 kb circular molecule has a number of features reminiscent of plastid DNAs. Sequence analysis shows that along with other genes the circle codes for 25 different tRNAs all of which are transcribed. Six of the tRNAs have some unusual features, and one has an intron, the only one found so far on the circle. Comparison of codon and anticodon usage indicates that the 25 tRNAs are sufficient to decode all the protein genes present on the circle. The maintenance of such a parsimonious but complete translation system is further evidence for the functionality of the circle.

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☐ 1: J Hepatol 1997 Oct;27(4):688-98 Related Article

ELSEVIER SCIENCE
FULL-TEXT ARTICLE

Identification of human liver carboxylesterase of the proteins involved in Plasmodium falciparum malaria sporozoite invasion in primary cultures human hepatocytes.

van Pelt JF, Moshage HJ, Depla E, Verhave JP, Yap

Department of Liver and Pancreatic Diseases, Universit Hospital Gasthuisberg, Leuven, Belgium.

BACKGROUND/AIMS: In a previous study, we have demonstrated that primary human hepatocytes in culture are susceptible for Plasmodium falciparum sporozoite invasion. For development of parasites into exo-erythrocytic forms. In a separate study we demonstrated the involvement of two liver plasma membrane proteins (55 kD and 20 kD) in the invasion of P. falciparum sporozoites in vitro. In this study we have unravelled the nature of the 55 kD protein. **METHODS:** For the identification of this protein, a 53-58 kD membrane protein fraction from human liver was isolated, radioactively labelled, incubated with sporozoites and cross-linked. After reduction of the cross-linker, the released proteins were separated with unlabelled 53-58 kD protein fraction and separated.

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TWO-dimensional SDS-PAGE. Autoradiography showed a spot corresponding to a protein of 55 kD and pI of 5.7-
RESULTS: Amino acid sequencing revealed the 55 kD pr carboxylesterase. The biological activity of purified hur carboxylesterase and of an antiserum against carboxyle on sporozoite invasion in vitro was evaluated. Human carboxylesterase as well as a rabbit antiserum against carboxylesterase inhibited the invasion of P. falciparum sporozoites into primary human hepatocytes in culture. number of carboxylesterase cDNA clones were isolated human liver cDNA library. Sequence analysis revealed tv different iso-types. Immunoaffinity purified recombina carboxylesterase was shown also to inhibit the invasion sporozoites into primary human hepatocytes. Immunocytochemical analysis of the localisation of carboxylesterase in primary cultures of human hepatocy using specific antibodies, showed its presence inside the hepatocytes and on the membrane. CONCLUSIONS: Carboxylesterase plays a role in the invasion process of falciparum sporozoites into human hepatocytes in vitro. implications of these findings are further discussed.

PMID: 9365045 [PubMed - indexed for MEDLINE]

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☐ 1: Gene 1997 Oct 24;200(1-2):91-8 Related Article

Entrez
PubMed

Partial nucleotide sequence and organisation of extrachromosomal plastid-like DNA in *Plasmodium berghei*.

Yap MW, Kara UA, ten Heggeler-Bordier B, Ting RC TM.

PubMed
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Molecular Parasitology Laboratory, School of Biological Sciences, Singapore, Singapore.

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The murine malaria parasite *Plasmodium berghei* contain plastid-like extrachromosomal genome. This genome is 3 size and is transcriptionally active as shown by RT-PCR. sequence analysis of the genome reveals 69.9-95.5% hom to sequences of the 35-kb extrachromosomal circle fou human malaria species *Plasmodium falciparum*. Homologo sequences include regions of genes for the ssu-rRNA, ls rpo B and clusters of t-RNAs. Sequence variation betwe two *Plasmodium* species exists in the non-coding intersp regions. A physical map has been constructed for the P. circle, indicating the EcoRI and HindIII restriction site as the arrangement of the rRNA, rpo B and tRNA genes Arrangement of these genes is similar to that found on falciparum 35-kb circle. The P. berghei circular element

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...distinct from the mitochondrial 6-kb DNA of both the i
and the human Plasmodium species. Preliminary results i
that the circle may be a useful target for drug therapy

PMID: 9373142 [PubMed - indexed for MEDLINE]

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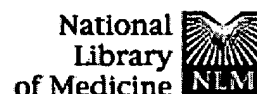
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Display Abstract Show: 20 Sort Send to

☐ 1: Acta Trop 1997 Oct 14;68(1):105-14 Related Article

ELSEVIER SCIENCE
FULL-TEXT ARTICLE

**Direct PCR amplification and sequence analysis
extrachromosomal Plasmodium DNA from dried
spots.**

Tan TM, Nelson JS, Ng HC, Ting RC, Kara UA.

Institute of Molecular and Cell Biology, National Univer:
Singapore, Singapore.

The Plasmodium parasite possesses two extrachromosor
genomes; the mitochondrial genetic element and the
extrachromosomal plastid-like DNA. The latter has only
fully described for one culture strain of *P. falciparum*. I
study, a rapid procedure for amplifying plastid DNA fro
blood spots of blood infected with different malaria sp
developed. PCR amplification of a 595 bp fragment with
plastid-like large subunit ribosomal-RNA (LSU-rRNA) ge
achieved using primers derived from the *P. falciparum* s
The PCR product was observed in all Plasmodium species
examined. Sequence analysis of amplified products hom
to an LSU-rRNA fragment of the plastid-like extrachro
circle revealed extensive conservation between Plasmoo
species including *P. falciparum*, *P. vivax*, *P. malariae* and l
hanchai

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PMID: 9352006 [PubMed - indexed for MEDLINE]

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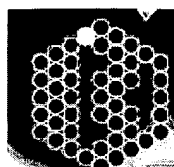
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Generic DB Entry Retrieval

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SV      U79731.1
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DE      tRNA-Thr, large subunit ribosomal RNA, tRNA-Met, tRNA-Arg, tRNA-Val,
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OC      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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RX      MEDLINE; 98038979.
RA      Yap M.W., Kara U.A., ten Heggeler-Bordier B., Ting R.C., Tan T.M.;
RT      "Partial nucleotide sequence and organisation of extrachromosomal
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RA      Yap M.W.C., Kara U.A.K., Tan T.M.C.;
RT      ;
RL      Submitted (26-NOV-1996) to the EMBL/GenBank/DDBJ databases.
RL      Institute of Molecular and Cell Biology, National University of Singapore,
RL      10 Kent Ridge Crescent S119260, Singapore
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Generic DB Entry Retrieval

ID AF182847 standard; DNA; INV; 594 BP.
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 XX
 DT 25-OCT-1999 (Rel. 61, Created)
 DT 25-OCT-1999 (Rel. 61, Last updated, Version 1)
 XX
 DE Plasmodium chabaudi from Australia large subunit ribosomal RNA gene,
 DE partial sequence.
 XX
 KW .
 XX
 OS Plasmodium chabaudi
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 XX
 RN [1]
 RP 1-594
 RA Tham J.M., Khoh L.K., Kara A.U.K.;
 RT ;
 RL Submitted (03-SEP-1999) to the EMBL/GenBank/DDBJ databases.
 RL Institute of Molecular and Cell Biology, 30 Medical Drive, Singapore
 RL 117609, Singapore
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Generic DB Entry Retrieval

ID U97561 standard; DNA; INV; 594 BP.
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 AC U97561;
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 SV U97561.1
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 DT 06-JAN-1999 (Rel. 58, Created)
 DT 20-MAR-2001 (Rel. 67, Last updated, Version 3)
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 DE partial sequence.
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 OS Plasmodium vivax (malaria parasite P. vivax)
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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 RP 1-594
 RX MEDLINE; 98013247.
 RX PUBMED; 9352006.
 RA Tan T.M.C., Nelson J.S., Ng H.C., Ting R.C.Y., Kara U.A.K.;
 RT "Direct PCR amplification and sequence analysis of extrachromosomal
 RT Plasmodium DNA from dried blood spots";
 RL Acta Trop. 68(1):105-114(1997).
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 RN [2]
 RP 1-594
 RA Tan T.M.C., Nelson J.S., Ng H.C., Ting R.C.Y., Kara U.A.K.;
 RT ;
 RL Submitted (15-APR-1997) to the EMBL/GenBank/DDBJ databases.
 RL Institute of Molecular and Cell Biology, National University of Singapore,
 RL 10 Kent Ridge Crescent S119260, Singapore
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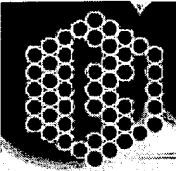
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Generic DB Entry Retrieval

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AC   AF182846;
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SV   AF182846.1
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DT   25-OCT-1999 (Rel. 61, Last updated, Version 1)
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DE   Plasmodium malariae from Burma large subunit ribosomal RNA gene, partial
DE   sequence.
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KW   .
XX
OS   Plasmodium malariae
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
XX
RN   [1]
RP   1-594
RA   Tham J.M., Khoh L.K., Kara A.U.K.;
RT   ;
RL   Submitted (03-SEP-1999) to the EMBL/GenBank/DDBJ databases.
RL   Institute of Molecular and Cell Biology, 30 Medical Drive, Singapore
RL   117609, Singapore
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SV  X75545.1
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DT  01-AUG-1994 (Rel. 40, Last updated, Version 3)
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KW  transfer RNA-Arg; transfer RNA-Asn; transfer RNA-Ile; transfer RNA-Leu;
KW  transfer RNA-Thr; transfer RNA-Val; trnA gene; trnI gene; trnL gene;
KW  trnM gene; trnN gene; trnR gene; trnT gene; trnV gene.
XX
OS  Plasmodium falciparum (malaria parasite P. falciparum)
OC  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
XX
RN  [2]
RP  1-5142
RA  Wilson R.J.M.;
RT  ;
RL  Submitted (02-NOV-1993) to the EMBL/GenBank/DDBJ databases.
RL  R.J.M. Wilson, National Institute for MEDical Research, Mill Hill, London
RL  NW7 1AA, UK
XX
RN  [3]
RA  Gardner M., Preiser P., Rangachari K., Moore D., Feagin D.,
RA  Williamson D.H., Wilson R.J.;
RT  "Nine duplicated tRNA genes on the plastid-like DNA of the malaria parasite
RT  Plasmodium falciparum";
RL  Gene 140:307-308(1994).
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Generic DB Entry Retrieval

ID PFCOMPIRA standard; DNA; INV; 15421 BP.
 XX
 AC X95275;
 XX
 SV X95275.1
 XX
 DT 29-JAN-1996 (Rel. 46, Created)
 DT 14-FEB-1997 (Rel. 50, Last updated, Version 24)
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 DE P.falciparum complete gene map of plastid-like DNA (IR-A)
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 KW LSU rRNA gene; ORF 101; ORF470; ORF51; rpoB gene; rpoC gene; rpoD gene;
 KW rps2 gene; SSU rRNA gene; tRNA-Ala; tRNA-Arg; tRNA-Asn; tRNA-Ile; tRNA-Leu;
 KW tRNA-Met; tRNA-Val.
 XX
 OS Plasmodium falciparum (malaria parasite P. falciparum)
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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 RA Wilson R.J.M., Denny P.W., Preiser P.R., Rangachari K., Roberts K., Roy A.,
 RA Whyte A., Strath M., Moore D.J., Moore P.W., Williamson D.H.;
 RT "Complete gene map of the plastid-like DNA of the malaria parasite
 RT Plasmodium falciparum";
 RL J. Mol. Biol. 261:155-172(1996).
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 RN [2]
 RP 1-15421
 RA Wilson R.J.M.;
 RT ;
 RL Submitted (23-JAN-1996) to the EMBL/GenBank/DDBJ databases.
 RL R.J.M. Wilson, National Institute for Medical Research, Mill Hill, London
 RL NW7 1AA, UK
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 DR SPTREMBL; Q25799; Q25799.
 DR SPTREMBL; Q25800; Q25800.
 DR SPTREMBL; Q25801; Q25801.
 DR SPTREMBL; Q25802; Q25802.
 DR SPTREMBL; Q25803; Q25803.
 DR SWISS-PROT; P21421; RPOB_PLAFA.
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 CC Related sequences X52177, X57167, X61660, X74308, X75544, and
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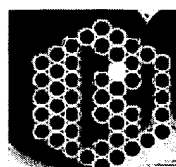
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ANALYSIS TOOLS

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Generic DB Entry Retrieval

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ID   PFLSRRN    standard; DNA; INV; 2700 BP.
XX
AC   X61660;
XX
SV   X61660.1
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DT   11-SEP-1991 (Rel. 29, Created)
DT   27-SEP-1995 (Rel. 45, Last updated, Version 22)
XX
DE   Plasmodium falciparum gene for a large subunit ribosomal RNA from the
DE   inverted repeat within the 35-Kb circular DNA
XX
KW   inverted repeat; ribosomal RNA; ribosomal RNA large subunit.
XX
OS   Plasmodium falciparum (malaria parasite P. falciparum)
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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RN   [1]
RP   1-2700
RA   Gardner M.J.;
RT   ;
RL   Submitted (22-AUG-1991) to the EMBL/GenBank/DDBJ databases.
RL   M.J. Gardner, Div of Parasitology, National Inst for Medical Research, The
RL   Ridgeway - Mill Hill, London NW7 1AA, UK
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RN   [2]
RP   1-2700
RX   MEDLINE; 93219063.
RA   Gardner M.J., Feagin J.E., Moore D., Rangachari K., Williamson D.H.,
RA   Wilson R.J.M.;
RT   "Sequence and organization of large subunit rRNA genes from the
RT   extrachromosomal 35-Kb circular DNA of the malaria parasite Plasmodium
RT   falciparum";
RL   Nucleic Acids Res. 21:1067-1071(1993).
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WEST Search History

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result set

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73	L1
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L2	L1 and (malar\$ or plasmodi\$).clm.
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2	L2
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L3	L2 and (detect\$ or determin\$ or measur\$ or hybridi\$)
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2	L3
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END OF SEARCH HISTORY

Done 1983

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<i>OP=AND</i>			
L1	berghei	446	L1
L2	L1 same plastid\$	0	L2
L3	L1 same (\$plastid)	0	L3
L4	L1 and (\$plastid or plastid\$)	2	L4
L5	(\$berghei or berghei\$)	831	L5
L6	L5 not l1	385	L6
L7	L6 and (\$plastid or plastid\$)	3	L7
L8	L7 not l4	3	L8

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☐ 1. Document ID: US 6313090 B1

L3: Entry 1 of 2

File: USPT

Nov 6, 2001

DOCUMENT-IDENTIFIER: US 6313090 B1

TITLE: Methods for treating parasitic infection using thiopeptides

Detailed Description Text (13):

The thiopeptides of the present invention can be administered to the subject in amounts sufficient to treat the parasitic infection in the subject as desired. Optimal dosages used will vary according to the individual and the particular parasitic infection, on the basis of age, size, weight, condition, etc, as well as the particular treatment effect being induced. One skilled in the art will realize that dosages are best optimized by the practicing physician and methods for determining dosage are described, for example, in Remington's Pharmaceutical Sciences (36).

Detailed Description Text (14):

In a preferred embodiment, the thiopeptide of the present invention can be administered to a human or a non-human animal in a pharmaceutically acceptable carrier in a dosage range of about 50 to 550 mg/kg/day and is preferably administered in a dosage of about 500 mg/kg/day. Treatment can be continued for an indefinite period of time, as indicated by monitoring of the signs, symptoms and clinical parameters associated with the parasitic infection according to protocols standard in the art for monitoring parasitic infections. Examples of the parameters that would be monitored can include, but are not limited to, amount and frequency of diarrheal excretion, oocyst excretion, culture of the parasite in body fluids and tissues, body weight and blood chemistry and urine analysis of hepatobiliary function. Oocyst excretion can be measured by quantitation of acid-fast stained stool specimens, ELISA antigen capture, immunofluorescence assay, DNA amplification, etc., according to protocols well known in the art.

Detailed Description Text (24):

Assay of Growth inhibition. Thiostrepton (1525 u/mg; Calbiochem) and anisomycin (Sigma) were dissolved at 100 mM in DMSO (Pierce). *P. falciparum* (strain 3D7) (44) was maintained in culture with human erythrocytes (5% hematocrit) in RPMI-1640 (Life Technologies) supplemented with HEPES and sodium bicarbonate and human sera (10%) under standard conditions (18,19). The growth inhibition assay was conducted as described (20). Briefly, the parasitemia was adjusted to 0.1% parasitemia, 2.5% hematocrit and 200 .mu.l aliquots placed in wells of a microtitre dish. Serial dilutions of drugs were made in RPMI. Thiostrepton was diluted to 10 mM in DMSO before the serial dilutions in RPMI. Aliquots (20 .mu.l) were added in triplicate to the cultures in the microtitre plate, mixing well. At the highest concentrations (final 0.2mM), thiostrepton precipitates. After incubation for 48 hours under standard conditions, [2,8-³H]-hypoxanthine Moravek Biochemicals, 12.5

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Ci/mmol) in RPMI (20 .mu.l, 0.05 mCi/ml) was added to each well. After incubation for a further 24 hours, the cultures were lysed and incorporated radioactivity was measured with an automated counter.

Detailed Description Text (26):

As of organelle and cytoplasmic transcript levels. RNA polymerase transcript levels were assessed by comparing the amounts of RNA synthesized at timepoints following drug treatment. Cultures of *P. falciparum* (3.2% parasitemia, 5% hematocrit) were treated with thiostrepton at 8 .mu.M and rifampin (Sigma) at 80 .mu.M; near the IC₅₀ values (this study and ref. 22). Aliquots (5 ml) of treated and control cultures were removed and immediately processed for RNA with a guanidinium thiocyanate solution, according to the manufacturer's directions (RNAagents, Promega). All RNA samples were dissolved in 50 .mu.l DEPC-treated water, DNase I treated as previously described (23) and an aliquot (1 .mu.l) was removed for RT-PCR. First strand synthesis of cDNA was completed with a random hexamer (Superscript Preamplification System, Life Technologies). One-tenth of the cDNA product was utilized for PCR of *rpoB/C*, *MSA1*, and *rRNA*. Primers corresponding to the 3' region of *rpoB*, 5'-GGGCTTTAGAAGCTTTTGG-3' (SEQ ID NO:1), and the 5' region of *rpoC*, 5'-CCATTTAAAATTGGTAATCCTG-3' (SEQ ID NO:2) were applied as described (2,3) for PCR of nascent *rpoB/C* transcripts. Reactions were cycled with the following parameters: 94.degree. C./30 seconds, 42.degree. C./30 seconds, 72.degree. C./60 seconds, 35 cycles. Primers for amplification of nucleotide 64 to 614 of *MSA1* with 5'-GTGTGATAATATTCATGG-3' (SEQ ID NO:3) and 5'-GGAGAGCATTTGGTG-3' (SEQ ID NO:4)(24) and the small subunit rRNA with oligonucleotides 841 and 844 (23) were used for amplification reactions following the parameters in the respective references except with 35 cycles. Samples were also analyzed after 25 cycles of amplification to ensure detection in the linear range of the amplification reaction, with similar results. Following electrophoresis of aliquots from the amplification reactions on 1% agarose:TBE gels, samples were transferred to nylon membranes (GeneScreen Plus, DuPont) and hybridized as described (25). The amplification products were probed with 5'-sup.32 P-labeled oligonucleotides. The *rpoB/C* products were probed with 5'-GTTTAGCTATTAATATAGAAGC-3' (SEQ ID NO:5) (nucleotide 2009-2030 of *rpoB*) and 5'-CGGAGAGGTATTAATACC-3' (SEQ ID NO:6) (nucleotide 108-125 of *rpoC*), in 5.times.SSC, 10 mM sodium phosphate, 0.05% sodium pyrophosphate, 1% sodium dodecyl sulfate, 5.times.Denhardt's solution, 100 .mu.g/ml yeast tRNA, 42.degree. C. and washed in the hybridization solution lacking Denhardt's and tRNA at 37.degree. C., three times. The final wash was 1.times.SSC, 0.5% sodium dodecyl sulfate, 42.degree. C. followed by autoradiography. The same results were obtained with either probe. The *MSA1* amplification products were similarly probed with 5'-AAACTTGTGTTCGGATATAG-3' (SEQ ID NO:7) and the rRNA products with oligonucleotide 842 (23).

Detailed Description Text (28):

The target of inhibition by thiostrepton. In the absence of a direct measure of plastid-like organelle protein synthesis, assay of mRNA levels by RT/PCR provides a sensitive assay for the selective effect of thiostrepton on the plastid-like organelle. The presence of a protein encoded by the organelle, identified in the 35-kb genome as a homolog of eubacterial RNA polymerase encoded by the *rpoB* and *rpoC* genes (5), was assayed during treatment. Selective inhibition of the plastid-like RNA polymerase with rifampin provides a comparison with the effect of thiostrepton, since prokaryotic RNA polymerases are sensitive to rifampin. The synthesis of the *rpoB/C* mRNA encoded by the 35-kb genome was then compared to a nuclear-encoded mRNA. On the basis that the 35-kb encoded *rpoB* and *rpoC* are transcribed as a polycistronic mRNA (3), nascent transcripts were assayed at various timepoints during drug treatment by RT/PCR of the mRNA including the intergenic spacer between *rpoB/C*. Also, the sensitivity of RT/PCR provides a relative estimate of the mRNAs corresponding to those encoded on the 35-kb genome versus those of nuclear-encoded mRNAs. Amplification of part of the mRNA corresponding with Merozoite Surface Antigen (*MSA1*) was chosen as a nuclear-encoded mRNA, as this is abundant in erythrocytic stages of *P. falciparum* (24). As a control, a section of nuclear-encoded SSU rRNA was also amplified as this is unaffected by antibiotics.

Detailed Description Text (35):

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Intact *C. parvum* oocyst assay 3.0.times.10.sup.4 *C. parvum* GCH1 oocysts per well were incubated in the above-mentioned concentrations of drug at 37.degree. C. (8% CO.sub.2) on confluent MDBKF5D2 cell monolayers in 96 well microtiter plates. The level of infection in each well was determined and analyzed by immunofluorescence assay at 48 hours, using *C. parvum* sporozoite rabbit anti-serum (0.1%) and fluorescein-conjugated goat anti-rabbit antibody (1.0%). Percent inhibition was calculated by subtracting the mean parasite/drug from the mean parasite/medium, divided by the mean parasite/medium, all of which was multiplied by 100. The analysis was performed using MCID and an inverted microscope.

Detailed Description Text (41):

Intact *C. parvum* oocyst assay . 3.0.times.10.sup.4 *C. parvum* GCH1 oocysts per well were incubated in the above-mentioned concentrations of drug at 37.degree. C. (8% CO.sub.2) on confluent MDBKF5D2 cell monolayers in 96 well microtiter plates. For some monolayers, the oocysts were incubated in DMEM on the cell monolayers for four hours, at which time the monolayers were washed and then drug was added to the wells. The level of infection in each well was determined and analyzed by immunofluorescence assay at 48 hours, using *C. parvum* sporozoite rabbit anti-serum (0.1%) and fluorescein-conjugated goat anti-rabbit antibody (1.0%). Percent inhibition was calculated by subtracting the mean parasite/drug from the mean parasite/medium, divided by the mean parasite/medium, all of which was multiplied by 100. The analysis was performed using MCID and an inverted microscope.

Detailed Description Text (47):

Intact *C. parvum* oocyst assay. 3.0.times.10.sup.4 *C. parvum* GCH1 oocysts per well were incubated in the above-mentioned concentrations of drug at 37.degree. C. (8% CO.sub.2) on confluent MDBKF5D2 cell monolayers in 96 well microtiter plates. The level of infection in each well was determined and analyze by immunofluorescence assay at 48 hours, using *C. parvum* sporozoite rabbit anti-serum (0.1%) and fluorescein-conjugated goat anti-rabbit antibody (1.0%). Percent inhibition was calculated by subtracting the mean parasite/drug from the mean parasite/medium, divided by the mean parasite/medium, all of which was multiplied by 100. The analysis was performed using MCID and an inverted microscope.

Detailed Description Text (51):

SCID mice (Taconic Farms, Germantown, N.Y.), preconditioned with monoclonal antibodies to interferon as described (41), were given an acute infection of *C. parvum* (10.sup.7 oocysts given orally). A total of five mice in two groups were used. One group received 500 mg/kg/day (in two doses of 250 mg/kg) of thiostrepton six days post-infection and the other group received a placebo. Treatment lasted ten days and oocyst shedding was measured by counting the number of oocysts in 30 fields under high power microscopy of acid-fast stained fecal smears and calculating the mean for each group as described (41). The results in FIG. 1 showed that thiostrepton significantly reduced oocyst shedding (shaded bars) compared to placebo (black bars). These data are summarized in Table 7. Mucosal scores describe the extent of mucosal infection detected in formalin-fixed sections of tissue samples from various gut sites (pyloric region of stomach, liver, gallbladder, mid-small intestine, terminal ileum, cecum and colon) taken during necropsy. Scoring was as follows: 0 (no infection) to 5 (maximal infection) and was expressed as the combined score of the number of gut sites examined.

CLAIMS:

1. A method for treating a parasitic infection in a subject infected with a parasite having a plastid-like organelle, comprising administering to the subject an infection treating amount of a thiopeptide in a pharmaceutically acceptable carrier, wherein the subject is a mammal.
4. The method of claim 3, wherein the parasite is selected from the group consisting of Plasmodium, Toxoplasma and Cryosporidium species.

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7. The method of claim 4, wherein the parasite is Plasmodium.

12. A method for treating Cryptosporidium infection in a subject infected with a parasite having a plastid-like organelle comprising administering to the subject an infection treating amount of a thiopeptide in a pharmaceutically acceptable carrier, wherein the subject is a mammal.

17. A method for treating a parasitic infection in a subject infected with a parasite having a plastid-like organelle, comprising administering to the subject an infection treating amount of a thiopeptide in a pharmaceutically acceptable carrier, wherein the parasitic infection is caused by a member of the Microspora phylum or Ascetospora phylum.

21. A method for treating a subject infected with a parasite comprising administering a thiopeptide to the subject, wherein the parasite is selected from the group consisting of Plasmodium, Toxoplasma, and Cryptosporidium.

22. The method of claim 21 wherein the parasite is Plasmodium.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw Desc
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☐ 2. Document ID: US 6268160 B1

L3: Entry 2 of 2

File: USPT

Jul 31, 2001

DOCUMENT-IDENTIFIER: US 6268160 B1

TITLE: Method of screening for anti-malarial compounds

Brief Summary Text (12):

(ii) determining whether the compound binds to or inhibits the protein, any such binding or inhibition being indicative that the compound is an anti-malarial.

Brief Summary Text (15):

(ii) determining whether the compound binds to said RNA or said fragment, any such binding being indicative that the compound is an anti-malarial.

Drawing Description Text (5):

FIG. 3A shows a Southern blot of endonuclease-restricted malarial genomic DNA hybridised with a PftufA-specific PCR product as probe. A single band for the 35 kb plastid was obtained for each restriction digest.

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Drawing Description Text (6):

FIG. 3B shows cross-hybridisation between endonuclease-restricted malarial genomic DNA and the yeast tufM gene, indicating the possible presence of a malarial version of tufM.

Drawing Description Text (13):

FIG. 11 shows slot blots of RNA fractionated on sucrose gradients. Pretreatment with anisomycin blocked the puromycin-induced shift of the hybridization signal for P.falciparum cytosolic 23S ribosomes but not the plastid 16S ribosomes. A-C. Blots hybridized with a probe for the cytosolic large subunit (23S) rRNA. Anisomycin blocked the puromycin-induced shift. D-F. The same blots hybridized with a probe for the plastid-encoded small subunit (16S) rRNA. Anisomycin did not block the puromycin-induced shift.

Drawing Description Text (14):

FIG. 12 is a slot blot showing the puromycin-induced shift of the hybridization signal for plastid mRNA specifying EF-Tu.

Drawing Description Text (15):

FIG. 13 contains immunoblots showing that binding of antibiotics modifies migration of EF-Tu.GDP in native polyacrylamide gels. Two segments of the same gel show A) heterologously expressed Pf EF-Tu.sub.pl protein detected with a malaria peptide-specific antibody and B) E.coli EF-Tu detected with a specific antibody (Breidenbach et al 1990). Lanes without antibiotics (1 and 5), lanes with 100 .mu.M antibiotic: GE2270A (2 and 6), enacyloxin IIa (3 and 7), kirromycin (4 and 8). Arrows indicate uncomplexed EF-Tu.

Detailed Description Text (25):

The invention includes an antibody specific for the EF-Tu protein of the invention. The antibody is preferably monoclonal, but may also be polyclonal. The antibody may be labelled. Examples of suitable antibody labels include radiolabels, biotin (which may be detected by avidin or streptavidin conjugated to peroxidase), alkaline phosphatase and fluorescent labels (e.g. fluorescein and rhodamine). The term "antibody" is used herein to include both complete antibody molecules and fragments thereof. Preferred fragments contain at least one antigen binding site, such as Fab and F(ab').sub.2 fragments. Humanised antibodies and fragments thereof are also included within the term "antibody".

Detailed Description Text (31):

Various different assay systems may be used to carry out the screening, but all the assays have in common that the EF-Tu protein of the invention is contacted with test compounds and the ability of each test compound to bind to or inhibit the protein is determined. Any such binding or inhibition is indicative that the compound could be useful as an anti-malarial drug.

Detailed Description Text (32):

The screening assays will generally require one or more controls. It will generally be desirable to include a positive control in the form of a compound known to bind to or inhibit the EF-Tu protein, so as to ensure that the assay system is responding properly. Examples of suitable positive controls include kirromycin (mocimycin) and aurodox (1-methylmocimycin), which we have shown through our experiments to be effective anti-malarials and which are known to inhibit prokaryotic EF-Tu. It will also generally be desirable to include a negative control in the form of a sample containing no test compound, so as to obtain a measurement of the background signal in the assay. If a test compound gives a signal in the assay above that of the background, this is indicative that the compound has given a positive result and could be an anti-malarial.

Detailed Description Text (33):

One convenient type of assay system is a "band shift" system. This involves determining whether a test compound advances or retards the EF-Tu protein of the invention on gel electrophoresis relative to the EF-Tu

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protein in the absence of test compound. The mobility of GDP complexed EF-Tu is decreased with GE2270A but increased with enacyloxin IIa or kirromycin.

Detailed Description Text (36):

(ii) determining the amount of the labelled reference compound that is bound to the protein; and

Detailed Description Text (37):

(iii) comparing the amount of bound labelled reference compound determined in step (ii) with the amount of said compound that binds to the protein in the absence of the test compound;

Detailed Description Text (39):

The amount of the labelled reference compound bound to the protein may be measured directly or indirectly. A direct measurement may be carried out by removing assay mixture containing the unbound labelled reference compound and measuring the amount of label that is in the protein fraction. Alternatively, the amount of labelled reference compound bound to the protein could be determined indirectly by measuring the amount of label remaining in the assay solution after removal of the protein fraction, which will be inversely related to the amount that has bound to the protein.

Detailed Description Text (40):

In a competitive binding assay system, the EF-Tu protein may be immobilised on a solid support or may be in solution. The use of immobilised protein has the advantage that, after the binding reaction is complete, the protein/labelled reference compound complex may be separated from the labelled reference compound that remains in solution by simply removing the solution away from the solid support. If, on the other hand, the protein is not immobilised during the assay but rather is in solution, then it will generally be necessary to devise a means for separating the protein/labelled reference compound complex from the uncomplexed reference compound before measuring the amount of label. Such separation could be achieved, for example, by precipitating the protein using an antibody to the protein or by using a non-specific protein precipitation technique.

Detailed Description Text (52):

This information allows the design of assays for screening for further anti-malarial compounds whose mechanism of action operates through the 23S rRNA. These assays involve contacting each of the test compounds with the 23S rRNA or a fragment thereof containing the GTPase binding domain, and measuring any binding of the test compounds to the rRNA or fragment. Any such binding is of course indicative that the compound could be an anti-malarial.

Detailed Description Text (53):

We have already developed one assay for detecting binding to the 23S rRNA. We made a short transcript from DNA encoding the 23S rRNA of the malaria plastid corresponding to the GTPase domain (about nucleotide 1051 to about nucleotide 1108) and found that the transcript bound thiostrepton strongly.

Detailed Description Text (55):

A screening assay for further anti-malarial compounds can be based on a competitive binding assay in which the ability of each test compound to compete with thiostrepton for binding to the Pf 23S rRNA.sub.pl is measured. Such an assay comprises

Detailed Description Text (57):

(ii) determining the amount of thiostrepton (or other reference compound) that is bound to the rRNA or the fragment; and

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Detailed Description Text (60):

In a screening assay based on the invention for further anti-malaria compounds, it would be necessary to use appropriate controls. A good positive control would be to use a compound known to compete with thiostrepton (or with the other reference compound) to ensure that the assay is working properly; a positive result for the known competitor in the assay would indicate that the assay had worked correctly. It would also generally be desirable to use a negative control comprising, for example, a sample in which no thiostrepton or test compound is present; this would enable the background signal in the assay to be determined and any signal above the background would indicate binding to the 23S rRNA.

Detailed Description Text (66):

In an experiment with RNase (Cox 1969), total polysomes were incubated with a range of concentrations of RNase (1-13 ng ml.^{sup.-1} ribosomes, Boehringer) prior to centrifugation for 30 min at 26.degree. C. In other experiments, polysomes were dissociated to monosomes and subunits by the incorporation of puromycin; here the total ribosome preparation was incubated for 20 min at 37.degree. C. with 2 mM puromycin in the "high salt" buffer to which was added 2 mM GTP, 10 .mu.l.ml.^{sup.-1} RNasin (39 U.mu.l.^{sup.-1}, Promega) and 1 mM DTT. In some experiments, ribosomes were incubated with both anisomycin (Sigma) and puromycin. Anisomycin was added at 3 mM for 10 min at 37.degree. C. followed by incubation with puromycin as above (Cundliffe et al 1974). After ribosome fractionation on the sucrose gradients, RNA was extracted with phenol/chloroform/isoamyl alcohol (Chomczynski et al 1987), precipitated in ethanol and blotted on to nylon membranes (Gene Screen, Trade Name) using a slot-blot apparatus (Scot-Labs). Hybridization was carried out with .sup.32 P-labelled DNA prepared from either cloned fragments of the 35 kb plDNA of P.falciparum, PCR products amplified from it, oligonucleotides based on its sequence (Wilson et al 1996), or with PCR products based on the sequence of Pf 28S cytosolic rRNA (McCutchen et al 1988). Hybridization signals were quantitated using a Molecular Dynamics phosphor imager.

Detailed Description Text (68):

EF-Tu model--Pf EF Tu.sub.pl was modelled by homology with the known 3D structures determined by X-ray crystallography of EF-Tu.GTP (Berchtold et al 1993) and EF-Tu.GDP (Polekhina et al 1996) both from Thermus aquaticus. Modelling was carried out with the WHAT-IF program package (Trade Name, Vriend 1990), as described in Tews et al 1996. Alignments had to be adjusted manually because of small gaps and insertions. An iterative procedure of the automated model-building algorithm checked and corrected the alignments until no errors were detectable. Three insertions in the Pf EF-Tu.sub.pl sequence had to be deleted: Leu 190, Pro263 and Leu359-Val363. The final alignment with the T. aquaticus structure had single residue gaps in the Pf sequence between Leu41 and Ser42 as well as residues Asn209 and Ile210. Co-ordinates for the C (alpha) backbone were copied from the known structure for overlapping segments and the atoms for the amino acids Gly, Ala and Pro were placed directly in their calculated positions. All remaining residues were assigned to Ala before the order in which side chains had to be placed was calculated by the algorithm implemented by the program. Atoms were subsequently placed using a position-dependent amino acid rotamer library. The model was refined geometrically and re-numbered according to the P.falciparum sequence.

Detailed Description Text (69):

Heterologous expression--The malarial plastid tufA gene was amplified by PCR, cloned into the TA vector (Trade Name, Invitrogen) and its sequence determined (Wilson et al 1996). Re-cloning into the expression vector pGEX (Trade Name, Pharmacia) was carried out with a PCR product generated using 5' and 3' primers providing custom-made restriction sites. Transfectants in E.coli (strains DH5 alpha, Sure, JM109) were found mostly to carry deletions within the tufA sequence, but one clone in JM109 contained the complete insert (sequenced on a single strand). This was expressed as a fusion protein of the expected size by induction of mid-log phase cultures with 50 .mu.M isopropyl-.beta.-D-thiogalactoside (IPTG) at 37.degree. C. or 27.degree. C. The insoluble fusion protein was solubilized in 5M guanidinium HCl and refolded by dilution (Lin et al 1991).

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Detailed Description Text (74):

Ribosomes from erythrocytic parasites were fractionated by centrifugation on linear gradients (20-50% sucrose) and RNA was extracted from fractions collected over the length of the gradients. Slot blots of the RNA were hybridized with ³²P-labelled DNA probes prepared from either cloned fragments of Pf plDNA, PCR products based on its sequence, or kinased oligonucleotides. As shown in FIG. 11 C&F, hybridization with probes for the large.sub.(cytosolic) or small.sub.(plastid) subunit rRNAs gave signals extending to the bottom of the gradient, indicative of rRNA incorporated in polysomes. Supportive evidence was obtained by limited digestion of the total ribosome preparation with RNase (13 ng RNase/mg ribosomes for 30 min at 26.degree. C.) before fractionation--this causes dissociation of the polysomes (Cox 1969) and shifted the hybridization signal up the gradient (data not shown). More specific evidence for a subset of polysomes belonging to the plastid compartment was obtained by incubating total ribosomes with 2 mM puromycin in the presence of GTP, 0.3M KCl and 1 mM DDT prior to density gradient fractionation: puromycin acts as an analogue of the 3' terminal adenosine of aminoacylated tRNAs and is incorporated into nascent peptide chains, terminating translation and dissociating polysomes (Gale et al 1981). Incubation with puromycin caused a shift of both the cytosolic and plastid rRNA hybridization signals up the gradient (FIG. 11, B&E). The specificity of the puromycin-shift was confirmed by pre-treating Pf ribosomes with the antibiotic anisomycin which binds only to eukaryotic ribosomes and prevents puromycin incorporation (Gale et al 1981). As shown in FIG. 11A, anisomycin blocked the puromycin-induced shift of the hybridization signal for Pf 28S cytosolic rRNA, whereas hybridization of the same blot with a probe for Pf 16S rRNA.sub.pl showed the puromycin-shift of the plastid subset of polysomes was not blocked (FIG. 11D).

Detailed Description Text (75):

Similar results were obtained with a probe for an mRNA specified by the plDNA. FIG. 12 shows the puromycin-induced shift of the hybridization signal for mRNA specifying EF-Tu.sub.pl.

Detailed Description Text (76):

To quantitate the relative proportions of the hybridization signals generated by different species of RNA, slot blots were hybridized with ³²P-labelled oligonucleotides, known amounts of DNA being used as appropriate standards. The 28S cytosolic rRNA was estimated to be 80-fold more plentiful than 16S rRNA_{pl} and 2000-fold more plentiful than the mRNA specifying EF-Tu.sub.pl (data not shown). These results and the puromycin-shifts are consistent with the presence of actively translating plastid ribosomes in blood cultures of malaria parasites.

Detailed Description Text (81):

When hybridized with a PftufA-specific PCR product under stringent conditions, Southern blots of endonuclease-restricted malarial genomic DNA gave a single band of the size predicted (FIG. 3A). At low stringency no other bands were revealed that might have corresponded to the nucleus-encoded mitochondrial gene tufM (Nagata et al, 1983; Wells et al. 1994). The likely presence of a malarial equivalent was indicated, however, by cross-hybridization at low stringency with a PCR product based on the yeast tufM gene (FIG. 3B).

Detailed Description Text (99):

The material tufA gene in pGEX was expressed as an insoluble fusion protein in E.coli JM 109. The protein was detected either with antibodies to the GST tag or with antibodies to a specific peptide sequence in domain I (IQKNKDYELIKSN SEQ ID NO:7) not found on E.coli EF-Tu. Washed inclusion bodies were dissolved and refolded by dilution (Lin et al 1991). This yielded a small amount of refolded protein that migrated in native acrylamide gels as a spontaneously cleaved product and we used this to show that the expressed protein forms complexes with kirromycin and other drugs that bind to different sites on EF-Tu. As shown in FIG. 13, the mobility (M.sub.r) of the expressed malarial protein was advanced or retarded in these complexes in the same characteristic way described for E.coli EF-Tu (Cetin et al 1996): the M.sub.r of the GDP form of the complex decreased with GE2270A, but increased with enacyloxin IIa or kirromycin. These results show that the

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heterologously expressed Pf EF-Tu.sub.pl can adopt a native conformation and bind the classical antibiotic inhibitors.

CLAIMS:

1. A method for screening a compound for anti-malaria activity with malaria elongation factor-Tu(EF-Tu) protein, which method comprises

(i) contacting the compound with the EF-Tu protein encoded on the 35 kb circular plastid DNA of Plasmodium falciparum; and

(ii) determining whether the compound binds to and inhibits the protein, any such binding and inhibition suggesting that the compound may have anti-malaria activity.

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